

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 15:04:42 ; Search time 1774.1 Seconds
(without alignments)
130.780 Million cell updates/sec

Title: us-09-532-263-6
Perfect score: 15
Sequence: 1 RCTCCAYTCRTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_ba3.*
- 4: gb_in1.*
- 5: gb_in2.*
- 6: gb_in3.*
- 7: gb_om.*
- 8: gb_ov.*
- 9: gb_pat1.*
- 10: gb_pat2.*
- 11: gb_ph.*
- 12: gb_pl1.*
- 13: gb_pl2.*
- 14: gb_pl3.*
- 15: gb_pl4.*
- 16: em_ba1.*
- 17: em_ba2.*
- 18: em_fun.*
- 19: em_htgo_hum.*
- 20: em_htgo_inv.*
- 21: em_htgo_rod.*
- 22: em_htg_hum1.*
- 23: em_htg_hum2.*
- 24: em_htg_hum3.*
- 25: em_htg_hum4.*
- 26: em_htg_hum5.*
- 27: em_htg_hum6.*
- 28: em_htg_hum7.*
- 29: em_htg_hum8.*
- 30: em_htg_inv1.*
- 31: em_htg_inv2.*
- 32: em_htg_other.*
- 33: em_htg_rod.*
- 34: em_hum1.*
- 35: em_hum2.*
- 36: em_hum3.*
- 37: em_hum4.*
- 38: em_hum5.*
- 39: em_hum6.*
- 40: em_hum7.*
- 41: em_in.*
- 42: em_om.*
- 43: em_or.*

- 44: em_ov.*
- 45: em_pat.*
- 46: em_ph.*
- 47: em_pl.*
- 48: em_ro.*
- 49: em_sts.*
- 50: em_sy.*
- 51: em_un.*
- 52: em_vi.*
- 53: gb_sts1.*
- 54: gb_sts2.*
- 55: gb_sts3.*
- 56: gb_sy.*
- 57: gb_un.*
- 58: gb_vil.*
- 59: gb_vi2.*
- 60: gb_htg1.*
- 61: gb_htg2.*
- 62: gb_htg3.*
- 63: gb_htg4.*
- 64: gb_htg5.*
- 65: gb_htg6.*
- 66: gb_htg7.*
- 67: gb_htg8.*
- 68: gb_htg9.*
- 69: gb_htg10.*
- 70: gb_htg11.*
- 71: gb_htg12.*
- 72: gb_htg13.*
- 73: gb_htg14.*
- 74: gb_htg15.*
- 75: gb_htg16.*
- 76: gb_htg17.*
- 77: gb_htg18.*
- 78: gb_htg19.*
- 79: gb_htg20.*
- 80: gb_htg21.*
- 81: gb_htg22.*
- 82: gb_htg23.*
- 83: gb_htg24.*
- 84: gb_htg25.*
- 85: gb_pr1.*
- 86: gb_pr2.*
- 87: gb_pr3.*
- 88: gb_pr4.*
- 89: gb_pr5.*
- 90: gb_pr6.*
- 91: gb_pr7.*
- 92: gb_pr8.*
- 93: gb_pr9.*
- 94: gb_rol.*
- 95: gb_rod.*
- 96: gb_in4.*
- 97: gb_pr10.*
- 98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	13.8	92.0	15	9 A70378	A70378 Sequence 8
c 2	13.8	92.0	21	10 AX095547	AX095547 Sequence
c 3	13.8	92.0	160	94 MUSAIC2A09	M94144 Mus musculu
c 4	13.8	92.0	207	94 MUSIL4R07	M64874 Mouse inter
c 5	13.8	92.0	213	91 D88111	D88111 Homo sapien
c 6	13.8	92.0	248	7 ECIL7R1	AF115754 Equus cab
7	13.8	92.0	367	54 G65440	G65440 stdJ388M5_1
c 8	13.8	92.0	403	93 HSIL7R5	AF043127 Homo sapi


```

Best Local Similarity 80.0%; Pred. NO. 7.9e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCCTCCA 15
Db 132 GCTCCACTCGCTCCA 118

RESULT 4
MUSILAR07/c MUSILAR07 207 bp DNA ROD 06-MAY-1996
LOCUS Mouse interleukin 4 receptor gene, exon 7.
DEFINITION M64874
ACCESSION M64874.1 GI:198354
VERSION interleukin 4 receptor.
KEYWORDS 7 of 12
SEGMENT Mus musculus (strain BALB/c, sub_species domesticus) DNA.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 207)
AUTHORS Wrighton,N., Campbell,L.A., Harada,N., Miyajima,A. and Lee,F.
TITLE The murine interleukin-4 receptor gene: genomic structure,
expression and potential for alternative splicing
JOURNAL Growth Factors 6 (2), 103-118 (1992)
MEDLINE 92265335
FEATURES
Source Location/Qualifiers
1..207
/organism="Mus musculus"
/strain="BALB/c"
/db_species="domesticus"
/db_xref="taxon:10090"
/cell_type="sperm"
<1..25
/note="putative"
/number=6
26..182
/standard_name="IL-4R'"
/note="approx. 1.4kb 3' of segment 6'; 'interleukin-4
receptor'; putative"
/number=7
/label=exon7
31
/note="comparing genomic to cDNA; found in Balb/c"
/replace="a"
183..207
/note="putative"
/number=7
45 a 52 c 55 g 55 t
BASE COUNT 45 a 52 c 55 g 55 t
ORIGIN
variation
intron
exon
intron
variation
intron
BASE COUNT 45 a 52 c 55 g 55 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 94; Length 207;
Best Local Similarity 80.0%; Pred. NO. 8e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCCTCCA 15
Db 160 ACTCCACTCACTCCA 146

RESULT 5
D88111/c D88111 213 bp DNA PRI 07-FEB-1999
LOCUS Homo sapiens DNA.
DEFINITION D88111
ACCESSION D88111.1 GI:1673297
VERSION Homo sapiens (strain:Hela) DNA, clone_lib:library of clones
KEYWORDS containing poly(dG)poly(dC)library clone:PHGC40L.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 213)
AUTHORS Nishikawa,N.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1996) to the DDBJ/EMBL/GenBank databases. Naoko
Nishikawa, Univ. Tokyo, Ins. Mol. Cell. Biosci.; Yayoi 1-1-1,
Bunkyo-ku, Tokyo 113, Japan (Tel:03-3812-2111(ex.7877),
Fax:03-3818-9437)
2 (bases 1 to 213)
AUTHORS Nishikawa,N., Oishi,M. and Kiyama,R.
TITLE Enrichment of poly(dG).poly(dC)-containing fragments from human
genomic DNA by Mg2+-dependent triplex affinity capture
JOURNAL Unpublished (1996)
AUTHORS Nishikawa,N., Kanda,N., Oishi,M. and Kiyama,R.
TITLE Enrichment of oligo(dG).oligo(dC)-containing fragments from human
genomic DNA by Mg 2+-dependent triplex affinity capture
JOURNAL Nucleic Acids Res. 25 (9), 1701-1708 (1997)
MEDLINE 97263793
FEATURES
Source Location/Qualifiers
1..213
/organism="Homo sapiens"
/strain="Hela"
/db_xref="taxon:9606"
/clone_lib="PHGC40L"
/cell_type="library of clones containing
poly(dG)poly(dC)library"
74 a 16 c 76 g 47 t
BASE COUNT 74 a 16 c 76 g 47 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 91; Length 213;
Best Local Similarity 80.0%; Pred. No. 8e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCCTCCA 15
Db 162 ACTCCATTCACCTCCA 148

RESULT 6
ECIL7R1 248 bp DNA MAM 28-NOV-1999
LOCUS Equus caballus interleukin-7 receptor (IL7R) gene, partial
DEFINITION sequence.
ACCESSION AF115754
VERSION AF115754.1 GI:6469582
KEYWORDS 1 of 2
SEGMENT 1 of 2
SOURCE horse.
ORGANISM Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
1 (bases 1 to 248)
AUTHORS Caetano,A.R., Lyons,L.A., Laughlin,T.F., O'Brien,S.J., Murray,J.D.
and Bowling,A.T.
TITLE Equine synteny mapping of comparative anchor tagged sequences
(CATS) from human Chromosome 5
JOURNAL Mamm. Genome 10 (11), 1082-1084 (1999)
MEDLINE 20028321
REFERENCE 2 (bases 1 to 248)
AUTHORS Caetano,A.R., Lyons,L.A., Laughlin,T.F., O'Brien,S.J., Murray,J.D.
and Bowling,A.T.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-1998) Veterinary Genetics Lab., University of
California Davis, One Shields Ave., Davis, CA 95616, USA
FEATURES
Source Location/Qualifiers
1..248
/organism="Equus caballus"
/db_xref="taxon:9796"
81 a 43 c 58 g 66 t
BASE COUNT 81 a 43 c 58 g 66 t
ORIGIN

```

Query Match 92.0%; Score 13.8; DB 7; Length 248;
 Best Local Similarity 80.0%; Pred. No. 8e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15
 :||||:|||||
 Db 19 ACTCCATTCCTCCA 5

RESULT 7
 LOCUS G65440 367 bp DNA STS 19-JUL-2000
 DEFINITION stdj388M5_151462 chromosome 22 genomic clone Homo sapiens STS
 genomic clone 388M5, sequence tagged site.
 ACCESSION G65440
 VERSION G65440
 KEYWORDS G65440.1 GI:9295650
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 367)
 AUTHORS Dawson, E., Chen, Y., Hunt, S. and Dunham, I.
 TITLE Extraction and analysis of SNP data from genomic sequence of human chromosome 22
 JOURNAL Unpublished (1999)
 COMMENT Synonyms: stSG73865
 Contact: Ian Dunham
 Sanger Centre
 The Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, UK
 Email: idl@sanger.ac.uk
 Primer A: GAAGTCGACGAGGGAACCTGC
 Primer B: GACTCAGACGAGGTCTGGA
 STS size: 367
 PCR Profile:

Presoak: 94 degrees C for 5.00 minutes
 Denaturation: 93 degrees C for 30 seconds
 Annealing: 60 degrees C for 30 seconds
 Extension: 72 degrees C for 30 seconds
 PCR Cycles: 35
 Final Extension 72 degrees C for 5 minutes
 Thermal Cycler: MJ Research (DNA Engine Tetrad)

Protocol:
 Template: 50-100 ng
 Primer: each 0.5 mM
 dNTPs: each 500 uM
 BSA: 170ug/ml
 2-mercaptoethanol: 10mM
 Taq Polymerase: 0.04 units/ul
 Total Vol: 15 ul

Buffer:
 6.7 mM MgCl2
 67 mM Tris-HCl
 16.7 mM (NH4)2SO4
 pH: 8.8

Accession of clone sequence : 297055.
 Location/Qualifiers
 1..367
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="388M5"
 /clone_lib="chromosome 22 genomic clone"
 1..367
 primer_bind 1..20
 primer_bind complement(348..367)
 BASE COUNT 76 a 121 c 96 g 74 t
 ORIGIN

Query Match 92.0%; Score 13.8; DB 54; Length 367;
 Best Local Similarity 80.0%; Pred. No. 8.2e+02;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCTCCAYTCRCTCCA 15
 :||||:|||||
 Db 337 ACTCCACTCACTCCA 351

RESULT 8
 LOCUS HSIL7R5/c 403 bp DNA PRI 05-DEC-1998
 DEFINITION Homo sapiens Interleukin-7 receptor precursor (IL7R) gene, exon 5.
 ACCESSION AF043127
 VERSION AF043127.1 GI:3978158
 KEYWORDS 5 of 7
 SEGMENT human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 403)
 AUTHORS Puel, A., Ziegler, S.F., Buckley, R.H. and Leonard, W.J.
 TITLE Defective IL7R expression in T(-)B(+)NK(+) severe combined immunodeficiency
 JOURNAL Nat. Genet. 20 (4), 394-397 (1998)
 MEDLINE 99057350
 REFERENCE 2 (bases 1 to 403)
 AUTHORS Puel, A., Ziegler, S.F., Buckley, R.H. and Leonard, W.J.
 TITLE Direct Submission
 JOURNAL Submitted (15-JAN-1998) Immunology, Virginia Mason Research Center,
 1000 Seneca St., Seattle, WA 98101, USA

FEATURES
 source 1..403
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 140..308
 /gene="IL7R"
 /number=5
 BASE COUNT 126 a 81 c 87 g 109 t
 ORIGIN

Query Match 92.0%; Score 13.8; DB 93; Length 403;
 Best Local Similarity 80.0%; Pred. No. 8.2e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCTCCAYTCRCTCCA 15
 :||||:|||||
 Db 265 ACTCCATTCCTCCA 251

RESULT 9
 LOCUS I21102/c 490 bp DNA PAT 07-OCT-1996
 DEFINITION Sequence 73 from patent US 5518880.
 ACCESSION I21102
 VERSION I21102.1 GI:1601456
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 490)
 AUTHORS Leonard, W.J., Noguchi, M. and McBride, O. Wesley.
 TITLE Methods for diagnosis of XSCID and kits thereof
 JOURNAL Patent: US 5518880-A 73 21-MAY-1996;
 FEATURES Location/Qualifiers
 1..490
 /organism="unknown"
 BASE COUNT 122 a 127 c 110 g 130 t 1 others
 ORIGIN

Query Match 92.0%; Score 13.8; DB 10; Length 490;
 Best Local Similarity 80.0%; Pred. No. 8.3e+02;

QY 1 RCTCCAYTCRCTCCA 15
 :||||:|||||
 Db 265 ACTCCATTCCTCCA 251

RESULT 9
 LOCUS I21102/c 490 bp DNA PAT 07-OCT-1996
 DEFINITION Sequence 73 from patent US 5518880.
 ACCESSION I21102
 VERSION I21102.1 GI:1601456
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 490)
 AUTHORS Leonard, W.J., Noguchi, M. and McBride, O. Wesley.
 TITLE Methods for diagnosis of XSCID and kits thereof
 JOURNAL Patent: US 5518880-A 73 21-MAY-1996;
 FEATURES Location/Qualifiers
 1..490
 /organism="unknown"
 BASE COUNT 122 a 127 c 110 g 130 t 1 others
 ORIGIN

Query Match 92.0%; Score 13.8; DB 10; Length 490;
 Best Local Similarity 80.0%; Pred. No. 8.3e+02;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCCTCCA 15
:|||||:|||||
Db 254 GCTCCATTCACCTCCA 240

RESULT 10
HUMIL2RG05/c
LOCUS HUMIL2RG05 490 bp DNA PRI 06-JAN-1995
DEFINITION Human interleukin 2 receptor gamma chain (IL2RG) gene, exon 5.
ACCESSION L12180
VERSION L12180.1 GI:307053
KEYWORDS interleukin 2 receptor gamma chain.
SEGMENT 5 of 8
SOURCE Homo sapiens (tissue library: Charon 4A) fetus liver DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)
Noguchi,M., Adelstein,S., Cao,X. and Leonard,W.J.
TITLE Characterization of the human interleukin-2 receptor gamma chain
gene
JOURNAL J. Biol. Chem. 268 (18), 13601-13608 (1993)
MEDLINE 93293887
FEATURES
Location/Qualifiers
1..490
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="fetus"
/tissue_type="liver"
/map="Xq13"
/order(L12179.1:221..423,1..125)
/gene="IL2RG"
/number=4
126..288
/gene="IL2RG"
/number=5

intron
exon
BASE COUNT 122 a 127 c 110 g 130 t 1 others
ORIGIN

Query Match 92.0%; Score 13.8; DB 97; Length 490;
Best Local Similarity 80.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 RCTCCAYTCRCCTCCA 15
:|||||:|||||
Db 254 GCTCCATTCACCTCCA 240

RESULT 11
CNS01DQR/c
LOCUS CNS01DQR 537 bp mRNA PLN 03-SEP-1999
DEFINITION Botrytis cinerea strain T4 cdna library under conditions of
nitrogen deprivation.
ACCESSION AL117163
VERSION AL117163.1 GI:5832379
KEYWORDS cdna library; nitrogen deprivation.
SOURCE Botryotinia fuckeliana.
ORGANISM Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
1 (bases 1 to 537)
Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
78026 Versailles, France
REFERENCE 2 (bases 1 to 537)
Genoscope.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :

CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The cdna library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
vector.

FEATURES
Location/Qualifiers
source
1..537
/organism="Botryotinia fuckeliana"
/strain="T4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W01G091"
BASE COUNT 137 a 46 c 178 g 176 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 14; Length 537;
Best Local Similarity 80.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 RCTCCAYTCRCCTCCA 15
:|||||:|||||
Db 265 ACTCCACTCACTCCA 251

RESULT 12
AC072998/c
LOCUS AC072998 572 bp DNA HTG 07-JUN-2000
DEFINITION Giardia intestinalis clone NJ4660 strain WB-C6, LOW-PASS SEQUENCE
SAMPLING.
ACCESSION AC072998
VERSION AC072998.1 GI:8325346
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Giardia intestinalis.
ORGANISM Giardia intestinalis
Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.
1 (bases 1 to 572)
Morrison,H.G., McArthur,A.G., Nixon,J., Eakin,N.Q., Kim,U.,
Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.
Giardia: a model for ancient eukaryotic genome analysis
Unpublished
2 (bases 1 to 572)
Nixon,J., Morrison,H.G., McArthur,A.G., Eakin,N.Q., Kim,U.,
Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.
Direct Submission
TITLE Submitted (07-JUN-2000) Josephine Bay Paul Center for Comparative
Molecular Biology and Evolution, Marine Biological Laboratory, 7
MBL Street, Woods Hole, MA 02543-1015, USA

COMMENT
* NOTE: This record contains 1 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 572: contig of 572 bp in length.
* Location/Qualifiers
1..572
/organism="Giardia intestinalis"
/strain="WB-C6"
/db_xref="taxon:5741"
/clone="NJ4660"

BASE COUNT 150 a 133 c 151 g 134 t 4 others
ORIGIN

Query Match 92.0%; Score 13.8; DB 74; Length 572;

Best Local Similarity 80.0%; Pred. No. 8.3e+02; Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15
:|||||:|||||
Db 311 GCTCCACTCACTCCA 297

RESULT 13

AC030504/c
LOCUS
DEFINITION
Giardia intestinalis clone E10461 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.

AC030504

VERSION

AC030504.1 GI:7385833

KEYWORDS

HTG; HTGS_PHASE0.

SOURCE

Giardia intestinalis.

ORGANISM

Giardia intestinalis.

Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.

1 (bases 1 to 585)

Morrison,H.G., McArthur,A.G., Nixon,J., Kim,U.,

Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.

Direct Submission

Submitted (02-APR-2000) Josephine Bay Paul Center for Comparative

Molecular Biology and Evolution, Marine Biological Laboratory, 7

MBL Street, Woods Hole, MA 02543-1015, USA

* NOTE: This record contains 1 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.

* 1

Location/Qualifiers

1..585

/organism="Giardia intestinalis"

/strain="WB-C6"

/db_xref="taxon:5741"

/clone="E10461"

E COUNT 144 a 140 c 150 g 145 t 6 others

ORIGIN

Query Match

Best Local Similarity 92.0%; Score 13.8; DB 71; Length 585;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15
:|||||:|||||
Db 76 GCTCCACTCACTCCA 62

RESULT 14

AF029294/c
LOCUS
DEFINITION
Mustela vison prolactin receptor (PRLr) mRNA, partial cds.

AC030504

AF029294.1 GI:2688974

KEYWORDS

American mink.

SOURCE

Mustela vison

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

gene

CDS

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

12; Conservative

3; Mismatches

0; Indels

0; Gaps

0;

QY

Db

RESULT

LOCUS

DEFINITION

AC030504

VERSION

AF029294.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

gene

CDS

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

12; Conservative

3; Mismatches

0; Indels

0; Gaps

0;

QY

Db

RESULT

LOCUS

DEFINITION

AC030504

VERSION

AF029294.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

gene

CDS

BASE COUNT

ORIGIN

1 (bases 1 to 652)
Douglas,D.A., Houde,A., Song,J.H., Farookhi,R., Concannon,P.W. and
Murphy,B.D.
Luteotropic hormone receptors in the ovary of the mink (Mustela
vison) during delayed implantation and early-postimplantation
gestation
Biol. Reprod. 59 (3), 571-578 (1998)
98384190
9716555

2 (bases 1 to 652)
Douglas,D.A., Song,J.H., Houde,A. and Murphy,B.D.
Direct Submission
Submitted (08-OCT-1997) Agriculture and Agri-Food Canada, Food
Research and Development Centre, 3600 Casavant Blvd. West,
St-Hyacinthe, Quebec J2S 8E3, Canada

Location/Qualifiers

1..652

/organism="Mustela vison"

/db_xref="taxon:9667"

/tissue_type="testis"

<1..>652

/gene="PRLr"

<1..>652

/gene="PRLr"

/codon_start=2

/product="prolactin receptor"

/protein_id="AAB8899.1"

/db_xref="GI:2688975"

/translation="KPGEDGGLPTKYTLTYHKEGETTTCEDPDYITSGPNSCYFNKKH
TSIMWYIITINATNMGSSSDPRVTITLYIVEPPPNVLSLELKQEDKKTYLWIK
WPTLVDRVSGMLTQIEIRLKPEKATEMTHFAGLQTFKILSLYPOCKYLVQVRC
KPDHGFVSEWSPKRSIQIPNDISMKDITVIMFVAVLSAVICLIIMAAVALKGHSMT"

BASE COUNT 195 a 159 c 145 g 153 t

ORIGIN

Query Match

Best Local Similarity 92.0%; Score 13.8; DB 7; Length 652;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15

Db 514 GCTCCACTCACTCCA 500

RESULT 15

AF169792/c

LOCUS

Ursus maritimus prolactin receptor mRNA, partial cds.

DEFINITION

AF169792

AC030504

VERSION

AF169792.1 GI:9988483

KEYWORDS

polar bear.

SOURCE

Ursus maritimus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

REFERENCE

1 (bases 1 to 681)

Howell-Skalla,L.A., Bunick,D., Bleck,G.T., Nelson,R.A. and

Bahr,J.M.

Cloning, sequence analysis, and seasonal mRNA expression of the

extracellular region of the luteinizing hormone receptor (LHR),

follicle-stimulating hormone receptor (FSHr), and prolactin

receptor (PRLr) genes in the testis of the black bear (Ursus

americanus)

Unpublished

2 (bases 1 to 681)

Howell-Skalla,L.A. and Bahr,J.M.

Direct Submission

Submitted (19-JUL-1999) Curriculum in Toxicology, University of

North Carolina, MD-72, US EPA, Research Triangle Park, NC 27711,

USA

Location/Qualifiers

1..681

Source

gene

CDS

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 80.0%; Score 13.8; DB 71; Length 585;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15

Db 76 GCTCCACTCACTCCA 62

RESULT 14

AF029294/c

LOCUS

DEFINITION

AF029294.1 GI:2688974

KEYWORDS

American mink.

SOURCE

Mustela vison

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.

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/organism="Ursus maritimus"
/db_xref="taxon:29073"
/tissue_type="liver"
1..22
<1..>681
/contig="PRLr"
/codon_start=1
/product="prolactin receptor"
/protein_id="AAG10648.1"
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/translation="RETFCKWKGEGDGLPTNYLTLYRKGEETTHECPDYISSGPN
SCYFNKKHTSIWMTYIIITINATNQMGSSSDPRYVDVTYIPEPDPVNLTLKLPQED
KPYLWMKWYPPTLVDRSGWLTQYEIRLKPKEATWETHFAGQQTQFKILSLYPGQ
KYLVOVRCKPDHGFSESPSSIQIPNDVTMKDTIVWIFVAVLSAVICLINVAVAL
KGHSMTVTCI"
primer_bind complement(662..681)
BASE COUNT 200 a 163 c 158 g 160 t
ORIGIN
Query Match 92.0%; Score 13.8; DB 7; Length 681;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 RCTCCAYTCRCTCCA 15
:||||:|||||
Db 537 GCTCCACTCACTCCA 523
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Search completed: August 29, 2001, 19:51:55
Job time: 17233 sec

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RESULT 15
AW165758      315 bp      mRNA      EST      12-NOV-1999
LOCUS      MBASBWA080M13R Ascaris suum (parasitic nematode) body wall muscle
DEFINITION      and hypodermis Ascaris suum cDNA clone MBASBWA080 5', mRNA
sequence.
ACCESSION      AW165758
VERSION      AW165758.1 GI:6382633
KEYWORDS      EST.
SOURCE      pig roundworm.
ORGANISM      Ascaris suum
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea
; Ascarididae; Ascaris.
REFERENCE      1 (bases 1 to 315)
AUTHORS      Daub,J., Geary,T. and Blaxter,M.
TITLE      A survey of genes expressed in the parasitic nematode Ascaris suum
JOURNAL      Unpublished (2000)
COMMENT      Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
3JT, UK.
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
The Ascaris suum EST dataset (including the ASC clustering
information) is available on the www at http://www.ed.ac.uk/(tilde.
)mbx/AscarisWeb/AscarisEST.html
PCR Primers
FORWARD: M13 Reverse (AGCGGATACAAATTCACACAGGA)
BACKWARD: M13 Forward (CGCCAGGGTTTCCCGATCAGCAGC)
Seq primer: M13 Reverse (AGCGGATACAAATTCACACAGGA).
FEATURES
source
1..315
/organism="Ascaris suum"
/db_xref="taxon:6253"
/clone="MBASBWA080"
/clone_lib="Ascaris suum (parasitic nematode) body wall
muscle and hypodermis"
/sex="mixed"
/tissue_type="body wall muscle and hypodermis"
/dev_stage="adult"
/note="Vector: Lambda Zap II; Site_1: NotI (5'end);
Site_2: NotI (3'end); Ascaris suum is an intestinal
nematode parasite of pigs. The library was constructed
from dissected body wall muscle and hypodermis tissue for
Dr. T. Geary, Pharmacia-Upjohn Inc, Kalamazoo, MI, USA
[tggeary@am.pnu.com]"
BASE COUNT      34 a 105 c 98 g 78 t
ORIGIN

Query Match      92.0%; Score 13.8; DB 112; Length 315;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RCTCCAYTCRCTCCA 15
       :|||||:|||||
Db      132 GCTCCATTCGCTCCA 146

Search completed: August 29, 2001, 19:22:10
Job time: 24133 sec

```


Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermotabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES

source

Location/Qualifiers
1. .297
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5930436B16"
/clone_lib="RIKEN full-length enriched, 13 days embryo
forelimb"
/sex="mixed"
/tissue_type="forelimb"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/notes="Site.1: Sali; Site.2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGAGTTAATTAATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end:
BamHI."

BASE COUNT 93 a 60 c 45 g 99 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 124; Length 297;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTCCATTCRCTCA 15
:|||||:|||||
Db 20 ACTCCATTCACCTCA 34

RESULT 12

BB024897

LOCUS

BB024897 299 bp mRNA EST 23-JUN-2000
DEFINITION RIKEN full-length enriched, adult male pituitary gland Mus
musculus cDNA clone 5330424007 3', mRNA sequence.

ACCESSION

BB024897

VERSION

BB024897.1 GI:8198974

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

EST.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 299)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
Y., Shigenoto,Y., Shinagawa,A., Shiraki,T., Soabe,Y., Sugahara,Y.
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya
T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamana,I.
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki

Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: +81-298-36-9013

Fax: +81-298-36-9098

Email: genome-res@rtc.riken.go.jp,

URL:http://genome.rtc.riken.go.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermotabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES

source

Location/Qualifiers

1. .299

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="5330424007"

/clone_lib="RIKEN full-length enriched, adult male
pituitary gland"

/sex="male"

/tissue_type="pituitary gland"

/dev_stage="adult"

/lab_host="DH10B"

/notes="Site.1: Sali; Site.2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 3.0 and subtraction to Rot = 100.0. Second strand
cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATTCGAGTTAATTAATTAATCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda

AF061117/c	AF061117	297 bp	mRNA	EST	06-MAY-1998
LOCUS	AF061117	Rice Milliyang 117 suspension culture	mRNA	Oryza sativa	
DEFINITION		cdna clone F25109, mRNA sequence.			

ACCESSION	AF061117
VERSION	AF061117.1
KEYWORDS	GI:3114679
SOURCE	EST.
ORGANISM	Oryza sativa.
	Oryza sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE	1 (bases 1 to 297)

Kim,C.Y., Cheon,S.Y. and Cho,M.J.
Isolation and Characterization of Fungal Ellicitor Responsive Rice
Genes by mRNA Differential Display
Unpublished (1998)
Contact: Kim, Cha Young
Biochemistry
PMBRC
900 Gajwa-dong, Chinju, Kyeong-nam 660-701, Korea
Email: choslab@ngae.gsnu.ac.kr.
Location/Qualifiers
1. .297
/organism="Oryza sativa"
/cultivar="Millyang 117"
/db_xref="taxon:4530"
/clone="F25109"
/clone_lib="Rice Millyang 117 suspension culture mRNA"
/note="suspension culture"

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BASE COUNT      77 a      66 c      70 g      84 t
ORIGIN

Query Match      92.0%      Score 13.8;      DB 14;      Length 297;
Best Local Similarity 80.0%;      Pred. No. 2.8e+03;
Matches 12;      Conservative 3;      Mismatches 0;      Indels 0;      Gaps 0;

Qy      1      RCTCCAYTCRCTCCA 15
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Db      78      ACTCCATTCACCTCCA 64

```

RESULT	11	
BB038288		
LOCUS	297 bp	mRNA
DEFINITION	BB038288 RIKEN full-length enriched, 13 days embryo forelimb Mus musculus cDNA clone 5930436B16 3' similar to U01135 Mus musculus B6D2f1 clone 2A-1 mRNA, mRNA sequence.	EST 23-JUN-2000
ACCESSION	BB038288	
VERSION	BB038288.1	GI:8444674
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 297)	
AUTHORS	Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirogane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,	

TITLE
JOURNAL
COMMENT

Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurlihara, C., Kusakabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
 Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata,
 Y., Shigemoto, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
 Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya,
 T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino,
 M., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Konno, H., et al.)
 Unpublished (2000)
 Contact: Yoshihide Hayashizaki
 Genome Exploration Research Group, Life Science Tsukuba Center.


```

Best Local Similarity 80.0%; Pred. No. 2.7e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 3;

QY 1 RCTCCAYTCRCTCCA 15
Db 16 ACTCCATTCCTCCA 30

RESULT 7
AW417497/c 275 bp mRNA EST 09-JUL-2000
LOCUS AW417497
DEFINITION 5A258 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AW417497
VERSION AW417497.1 GI:6945379
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 275)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keeler,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR primers
FORWARD: AGAACAACGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 20 row: K column: 3
Seq primer: ATTAGTGACACTATAG.
FEATURES
Location/Qualifiers
source 1..275
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 65 a 59 c 83 g 66 t 2 others
ORIGIN
Query Match 92.0%; Score 13.8; DB 115; Length 275;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15
Db 64 GCTCCATTCCTCCA 50

RESULT 8
AA562009/c 287 bp mRNA EST 18-AUG-1997
LOCUS AA562009
DEFINITION v12lq04_r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:972918 5' similar to gb:M29697 Mouse interleukin-7 receptor
(MOUSE); mRNA sequence.
ACCESSION AA562009
VERSION AA562009.1 GI:2333474
KEYWORDS EST.
SOURCE house mouse.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 287)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,F., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:553646
Putative full length read
vector to vector length is 288
Seq primer: -28ml3 revl ET from Amersham.
FEATURES
Location/Qualifiers
source 1..287
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:972918"
/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/notes="Organ: blood; Vector: pBluescript SK-; Site.1:
EcoRI; Site.2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGCAGG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT 84 a 70 c 59 g 74 t
ORIGIN
Query Match 92.0%; Score 13.8; DB 9; Length 287;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15
Db 160 ACTCCACTCGCTCCA 146

RESULT 9
BB024272/c 295 bp mRNA EST 23-JUN-2000
LOCUS BB024272
DEFINITION RIKEN full-length enriched, adult male pituitary gland Mus
musculus cDNA clone 5330420L02 3', mRNA sequence.
ACCESSION BB024272
VERSION BB024272.1 GI:8197502
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 295)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Soabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya

```

Matches	12;	Conservative	3;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	RCCTCAATTCRCTCCA	15						
Db	107	ACTCCACTCGCTCCA	121						
RESULT	5								
LOCUS	AQ548570/c								
DEFINITION	CITBI-El-2635F16.TF CITBI-El Homo sapiens genomic clone 2635F16, DNA sequence.								
ACCESSION	AQ548570								
VERSION									
KEYWORDS	GSS.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	1 (bases 1 to 256)								
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C								
TITLE	Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building								
JOURNAL	Unpublished (1997)								
COMMENT	Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html. Seq primer: MJ3-21 Class: BAC ends.								
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	/db_xref="taxon:9606"								
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	/sex="male"								
	/cell_type="sperm"								
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BASE COUNT									
ORIGIN									
Query Match	92.0%;								
Best Local Similarity	80.0%;								
Matches	12;	Conservative	3;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	RCCTCAATTCRCTCCA	15						
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RESULT	6								
LOCUS	BB051888								
DEFINITION	BB051888 RIKEN full-length enriched, 12 days embryo male wolffian duct Mus musculus cDNA clone 6720436D12 3' similar to U01135 Mus musculus B6D2F1 clone 2A-1 mRNA, mRNA sequence.								
ACCESSION	BB051888								
VERSION									
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
REFERENCE	1 (bases 1 to 256)								
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C								
TITLE	Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building								
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Matches	12;	Conservative	3;	Mismatches	0;	Indels	0;	Gaps	0;
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BASE COUNT									
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LOCUS	BB051888								
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REFERENCE	1 (bases 1 to 256)								
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C								
TITLE	Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building								
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source	1. .256								
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BASE COUNT									
ORIGIN									
Query Match	92.0%;								

v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCACGTCACGACG

Plate: 40 row: J column: 24

Seq primer: ATTAGTGACACTATAG.

FEATURES

source Location/Qualifiers

1. .173

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

BASE COUNT 26 a 38 c 59 g 50 t

ORIGIN

Query Match 92.0%; Score 13.8; DB 151; Length 173;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15

:||||:|||||

Db 23 GCTCCATTCACCTCCA 9

RESULT 3

BE076128/c

LOCUS

DEFINITION MR2-BT0590-100300-118-c08_1 BT0590 Homo sapiens cDNA, mRNA

201 bp mRNA EST 09-JUN-2000

sequence.

ACCESSION BE076128

VERSION BE076128.1

KEYWORDS GI:8425639

SOURCE EST.

ORGANISM human.

REFERENCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 201)

Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-MR2-BT0590-100

300-118-c08_1&t3=2000-03-10&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 201.

Location/Qualifiers

1. .201

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="BT0590"

Query Match 92.0%; Score 13.8; DB 21; Length 248;

Best Local Similarity 80.0%; Pred. No. 2.7e+03;

/dev_stage="Adult"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the puc 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 30 a 50 c 71 g 50 t

ORIGIN

Query Match 92.0%; Score 13.8; DB 163; Length 201;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15

:||||:|||||

Db 43 GCTCCACTCACTCCA 29

RESULT 4

AI505954

LOCUS

DEFINITION

AI505954 248 bp mRNA EST 11-MAR-1999

VI21f12.x1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone

(IMAGE:972911 3' similar to gb:M29697 Mouse interleukin-7 receptor

(MOUSE)); mRNA sequence.

ACCESSION AI505954

VERSION AI505954.1

KEYWORDS GI:4403805

SOURCE EST.

ORGANISM house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 248)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter

, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

CONTACT: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:553639

This clone was previously sequenced on the 5' end only, this new

data is from the 3' end

Location/Qualifiers

1. .248

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:972911"

/clone_lib="Stratagene mouse Tcell 937311"

/tissue_type="Tcell"

/dev_stage="M30 CD4+ cells"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: blood; Vector: pBluescript SK-; Site_1:

ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:

Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACCAG

3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'.

BASE COUNT 63 a 49 c 60 g 76 t

ORIGIN

MEDLINE COMMENT

9704477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
Oligo-dT track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA-No.

FEATURES source

Location/Qualifiers
1..151
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="NIH_BMAP_MHI2_S1"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; the
NIH_BMAP_MHI2_S1 library is a subtracted library derived
from NIH_BMAP_MHI2. NIH_BMAP_MHI2 is a library derived
from mouse hippocampus tissue. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu.
TAG_SEQ=None found"
31 a 48 g 38 t

BASE COUNT ORIGIN

31 a 48 g 38 t

Query Match 92.0%; Score 13.8; DB 149; Length 151;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCCTCCA 15

DB 101 ACTCCACTCGCTCCA 87

RESULT 2

BF601415/c 173 bp mRNA EST 13-DEC-2000
LOCUS BF601415 MARC 3BOV BOS taurus cDNA 5', mRNA sequence.
DEFINITION BF601415
ACCESSION BF601415.1 GI:11698637
VERSION BF601415.1
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 173)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid
W.W. and Keele, J.W.

Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

JOURNAL COMMENT

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	13.8	92.0	151	149	BF458328	UI-M-BZ1-1
C 2	13.8	92.0	173	151	BF601415	266391 MA
C 3	13.8	92.0	201	163	BE076128	MR2-BT059
C 4	13.8	92.0	248	21	AI505954	V121f12.x
C 5	13.8	92.0	256	230	AQ548570	CITBI-EI-
C 6	13.8	92.0	258	124	BB051888	BB051888
C 7	13.8	92.0	275	115	AW147497	AW147497 54258 MAR
C 8	13.8	92.0	287	9	AA562009	V121q04.r
C 9	13.8	92.0	295	123	BB024272	BB024272
C 10	13.8	92.0	297	14	AF061117	AF061117 AF061117
C 11	13.8	92.0	297	124	BB038288	BB038288
C 12	13.8	92.0	299	123	BB024897	BB024897
C 13	13.8	92.0	302	28	AV298115	AV298115
C 14	13.8	92.0	313	235	AQ937634	NB6-223C
C 15	13.8	92.0	315	112	AW165758	MBASBWA08
C 16	13.8	92.0	331	111	AW057700	AW057700 wx02c04.x
C 17	13.8	92.0	335	190	W23972	W23972 zb47a01.r1
C 18	13.8	92.0	338	148	BF425404	BF425404 su43c09.y
C 19	13.8	92.0	341	2	AA083143	zn08b04.r
C 20	13.8	92.0	341	13	AA921043	vv75h06.r
C 21	13.8	92.0	343	138	BE685591	187957 MA
C 22	13.8	92.0	349	115	AW17922	AW17922 52777 MAR
C 23	13.8	92.0	353	30	AV406268	AV406268
C 24	13.8	92.0	356	136	BE517357	BE517357 WHE0625.D
C 25	13.8	92.0	360	9	AA621766	af06d10.s
C 26	13.8	92.0	365	230	AQ545960	CITBI-EI-
C 27	13.8	92.0	366	150	BF524586	BF524586 UI-R-AD0-
C 28	13.8	92.0	376	111	AW074425	AW074425 xa93a07.x
C 29	13.8	92.0	376	222	FR0029534	AL025903 Fugu rubr
C 30	13.8	92.0	389	115	AW406187	AW406187 UI-HF-BL0
C 31	13.8	92.0	396	154	BG516644	ECESd59
C 32	13.8	92.0	407	231	AQ669609	HS 5364.A
C 33	13.8	92.0	413	22	AI633127	t219d11.x
C 34	13.8	92.0	413	154	BG516645	ECESd59
C 35	13.8	92.0	419	151	BF599654	263517 MA
C 36	13.8	92.0	422	170	BF880060	IL3-ET011
C 37	13.8	92.0	427	110	AW005961	w280a07.x
C 38	13.8	92.0	430	170	BF880064	IL3-ET011
C 39	13.8	92.0	436	150	BF559553	UI-R-AI-d
C 40	13.8	92.0	438	142	BE926519	MR4-BT039
C 41	13.8	92.0	441	234	AQ813137	AQ813137 HS 5300.A
C 42	13.8	92.0	443	13	AA909507	o116d11.s
C 43	13.8	92.0	446	110	AW001800	AA001800 ws05c01.x
C 44	13.8	92.0	458	1	AA043001	AA043001 zk56f01.r
C 45	13.8	92.0	459	22	AI559567	tq50f02.x

ALIGNMENTS

RESULT 1
BF458328/c 151 bp mRNA EST 01-DEC-2000
LOCUS BF458328
DEFINITION UI-M-BZ1-blp-e-08-0-UI.s1 NIH_BMAP_MHI2_S1 Mus musculus cDNA clone
UI-M-BZ1-blp-e-08-0-UI 3', mRNA sequence.
ACCESSION BF458328
VERSION BF458328.1 GI:11524497
KEYWORDS EST.
SOURCE house musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 151)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

117: gb_est48:*
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256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 12:39:57 ; Search time 3770.35 seconds
(without alignments)
37.607 Million cell updates/sec

Title: US-09-532-263-6
Perfect score: 15
Sequence: 1 RCTCCAYTCRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *
12: gb_est12: *
13: gb_est13: *
14: gb_est14: *
15: gb_est15: *
16: gb_est16: *
17: gb_est17: *
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110: gb_est41: *
111: gb_est42: *
112: gb_est43: *
113: gb_est44: *
114: gb_est45: *
115: gb_est46: *
116: gb_est47: *

PT for diagnosis or detection

XX

PS Claim 10; Page 46; 69pp; English.

XX

CC The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.

XX

SQ Sequence 465 BP; 158 A; 79 C; 92 G; 135 T; 1 other;

Query Match

Best Local Similarity 92.0%; Score 13.8; DB 19; Length 465;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Caps 0;

Qy 1 RCTCCAYTCRCTCCA 15

:|||||:|||||

Db 185 ACTCCACTCACTCCA 171

Search completed: August 29, 2001, 20:16:40
Job time: 7421 sec

XX This sequence represents a PCR amplified fragment of the mouse
CC haemopoietin receptor protein family NR8 gene. The sequence was used to
CC isolate further mouse NR8 genes. Antibodies to the NR8 family proteins
CC are used for the diagnosis of blood formation disorders. Compounds
CC identified as binding to the proteins are used for the treatment of
CC such disorders.
XX
SQ Sequence 330 BP; 72 A; 96 C; 94 G; 68 T; 0 other;

Query Match 92.0%; Score 13.8; DB 21; Length 330;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCCTCCA 15
Db 297 ACTCCATTCACCTCCA 283

RESULT 14
AA89731/c
ID AA89731 standard; cDNA; 444 BP.
XX
AC AA89731;
XX
DT 08-JAN-2001 (first entry)
XX
DE Mouse IL-3 receptor nucleotide sequence #2.
XX
KW Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic;
KW antiallergic; antiasthmatic; nootropic; neuroprotective; anticonvulsant;
KW vulnerable; asthma; inflammation; allergy; Chediak-Higashi syndrome; CHS;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
KW digestion disorder; wound healing disorder; gene therapy; ss.
XX
OS Mus sp.
XX
PN WO200043419-A2.
XX
PD 27-JUL-2000.
XX
PF 20-JAN-2000; 2000WO-US01431.
XX
PR 20-JAN-1999; 99US-0116534.
PR 26-JAN-1999; 99US-0117274.
PR 26-JAN-1999; 99US-0117308.
PR 26-JAN-1999; 99US-0117309.
PR 26-JAN-1999; 99US-0117312.
PR 01-FEB-1999; 99US-0118177.
PR 01-FEB-1999; 99US-0118178.
PR 01-FEB-1999; 99US-0118179.
PR 09-FEB-1999; 99US-0119286.
PR 11-FEB-1999; 99US-0119998.
PR 11-FEB-1999; 99US-0119759.
XX
PA (RIGE-), RIGEL PHARM INC.
XX
PI Luo Y;
XX
DR WPI; 2000-482908/42.
XX
PT New nucleic acids encoding Exo proteins which are useful in the
PT diagnosis, treatment or prevention of exocytosis-mediated disorders
PT such as asthma, inflammation and allergies -
XX
PS Disclosure; Page 301-302; 305pp; English.
XX
CC The present sequence encodes a polypeptide which is associated with
CC the exocytosis pathway. cDNA molecules encoding proteins involved in
CC exocytosis have been isolated by yeast one-hybrid and two-hybrid
CC screening. Novel proteins, termed Exo proteins, have been identified that
CC interact with known exocytosis-associated proteins such as GS27, alpha

CC snap, unc18-1, vamp3, snap-23, and the rab family of proteins.
CC Exo proteins and their agonists and antagonists are useful in the
CC diagnosis, treatment or prevention of exocytosis-mediated disorders
CC such as asthma, inflammation, allergies, Chediak-Higashi Syndrome
CC (CHS), Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC diabetes, digestion disorders and wound healing disorders.
CC The nucleic acids, antagonists or agonists of Exo proteins are useful
CC in gene therapy. The nucleic acids are also useful for generating
CC transgenic or knock-out animals which can be used in the
CC development and screening of therapeutically useful reagents.
XX
SQ Sequence 444 BP; 124 A; 115 C; 115 G; 87 T; 3 other;

Query Match 92.0%; Score 13.8; DB 21; Length 444;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCCTCCA 15
Db 249 GCTCCACTCGCTCCA 235

RESULT 15
AAV22698/c
ID AAV22698 standard; DNA; 465 BP.
XX
AC AAV22698;
XX
DT 24-SEP-1998 (first entry)
XX
DE Interleukin-13 binding protein C-terminal region gene.
XX
KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 1..465
FT /*tag= a
FT /product= "IL-13 binding protein Open Reading Frame 1"
FT /note= "No start codon, stop codons given within
FT sequence."
FT CDS
FT 2..463
FT /*tag= b
FT /product= "IL-13 binding protein ORF 2"
FT /note= "No start codon, stop codons given within
FT sequence."
FT CDS
FT 3..455
FT /*tag= c
FT /product= "IL-13 binding protein ORF 3"
FT /note= "No start codon, stop codons given within
FT sequence."
XX
PN WO9810638-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-AU00591.
XX
PR 27-FEB-1997; 97AU-0005374.
PR 10-SEP-1996; 96AU-0002262.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX
DR WPI; 1998-207062/18.
DR P-FSDB; AAW56255, AAW56256, AAW56257.
XX
PT New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or

KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
 KW PCR; primer; amplification; Human.
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9811225-A2.
 PD 19-MAR-1998.
 XX
 XX 11-SEP-1997; 97WO-GB02479.
 XX 11-SEP-1996; 96AU-0002246.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIEGLEWSKA H E.
 XX Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y;
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T;
 PI Zhang J;
 XX WPI: 1998-260970/23.
 DR New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 XX Example 16; Page 66; 182pp; English.
 XX The probe AAV27166 and primers AAV27167-V27168 were used in a method of
 CC the invention to isolate NR6 a novel haemopoietin receptor (HR).
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and
 CC its derivatives can be used for modulating the activity of the receptors
 CC e.g. to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present
 CC in therapeutics used for modulating neuronal proliferation,
 CC differentiation and survival. The products can also be used for
 CC detection and diagnosis, e.g. for cancers or predisposition to cancers,
 CC or for drug screening.
 XX
 SQ Sequence 18 BP; 3 A; 8 C; 4 G; 3 T; 0 other;
 Query Match 92.0%; Score 13.8; DB 19; Length 18;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCTCCAYTCRCTCCA 15
 :|||||:|||||
 Db 2 gctccactgcgtcca 16
 RESULT 10
 AAF95960/c
 ID AAF95960 standard; DNA; 21 BP.
 XX
 AC AAF95960;
 XX
 DT 06-JUN-2001 (first entry)
 XX Human gene single nucleotide polymorphism #721.
 DE
 XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Variation replace(11,T)
 /*tag= a

FT /standard_name= "single nucleotide polymorphism"
 XX WO200118250-A2.
 PN
 XX 15-MAR-2001.
 PD
 XX 07-SEP-2000; 2000WO-US24503.
 PF
 XX 10-SEP-1999; 99US-0153357.
 PR 26-JUL-2000; 2000US-0220947.
 PR 16-AUG-2000; 2000US-0225724.
 XX (WBED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, McCarthy JJ;
 PI WPI: 2001-226749/23.
 DR Nucleic acids comprising single nucleotide polymorphisms, useful in
 XX applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis -
 XX Examples: Page 98; 242pp; English.
 PS The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification.
 XX Sequence 21 BP; 4 A; 2 C; 11 G; 4 T; 0 other;
 SQ
 Query Match 92.0%; Score 13.8; DB 22; Length 21;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCTCCAYTCRCTCCA 15
 :|||||:|||||
 Db 20 ACTCCACTCGCTCCA 6
 RESULT 11
 AAT96787/c
 ID AAT96787 standard; cDNA; 25 BP.
 XX
 AC AAT96787;
 XX
 DT 30-MAR-1998 (first entry)
 XX Human and macaque 2cytor2 cytokine receptor primer ZG9803.
 DE
 XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 KW infertility; antagonist; contraceptive; diagnostic; therapeutic;
 KW primer; ss.
 XX Synthetic.
 OS OS Homo sapiens.
 OS Macaque sp.
 XX WO9733913-A1.
 PN
 XX 18-SEP-1997.
 PD
 XX 12-MAR-1997; 97WO-US04043.

CC haemopoietin receptor protein family NR8 genes. The NR8 family
 CC sequences were initially searched for comparison on a nucleic acid
 CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
 CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 CC AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
 CC sequences used in the search. Antibodies to the NR8 family proteins are
 CC used for the diagnosis of blood formation disorders. Compounds identified
 CC as binding to the proteins are used for the treatment of such disorders.
 XX
 SQ Sequence 15 BP; 3 A; 0 C; 8 G; 4 T; 0 other;

Query Match 92.0%; Score 13.8; DB 21; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15
 :||||:|||||
 Db 15 ACTCCACTCACTCCA 1

RESULT 7
 AAZ90893/c
 ID AAZ90893 standard; DNA; 15 BP.

XX AC AAZ90893;

XX DT 24-MAY-2000 (first entry)

XX DE Human NR8 gene probe #121.

XX KW Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder; fusion protein; probe; ss.

XX OS Homo sapiens.

XX PN WO9967290-A1.

XX PD 29-DEC-1999.

XX PF 23-JUN-1999; 99WO-JP03351.

XX PR 24-JUN-1998; 98JP-0214720.

XX PR 19-OCT-1998; 98JP-0297409.

XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX PI Nomura H, Maeda M;

XX DR WPI; 2000-116933/10.

XX PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders -

XX PS Example 1; Page 44; 176pp; Japanese.

XX CC The invention relates to the isolation of sequences encoding human
 CC haemopoietin receptor protein family NR8 genes. The NR8 family
 CC sequences were initially searched for comparison on a nucleic acid
 CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
 CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 CC AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
 CC sequences used in the search. Antibodies to the NR8 family proteins are
 CC used for the diagnosis of blood formation disorders. Compounds identified
 CC as binding to the proteins are used for the treatment of such disorders.
 XX
 SQ Sequence 15 BP; 3 A; 1 C; 8 G; 3 T; 0 other;

Query Match 92.0%; Score 13.8; DB 21; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15
 :||||:|||||
 Db 15 ACTCCACTCACTCCA 1

RESULT 8
 AAZ90894/c
 ID AAZ90894 standard; DNA; 16 BP.

XX AC AAZ90894;

XX DT 24-MAY-2000 (first entry)

XX DE Human NR8 gene probe #122.

XX KW Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder; fusion protein; probe; ss.

XX OS Homo sapiens.

XX PN WO9967290-A1.

XX PD 29-DEC-1999.

XX PF 23-JUN-1999; 99WO-JP03351.

XX PR 24-JUN-1998; 98JP-0214720.

XX PR 19-OCT-1998; 98JP-0297409.

XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX PI Nomura H, Maeda M;

XX DR WPI; 2000-116933/10.

XX PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders -

XX PS Example 1; Page 44; 176pp; Japanese.

XX CC The invention relates to the isolation of sequences encoding human
 CC haemopoietin receptor protein family NR8 genes. The NR8 family
 CC sequences were initially searched for comparison on a nucleic acid
 CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
 CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 CC AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
 CC sequences used in the search. Antibodies to the NR8 family proteins are
 CC used for the diagnosis of blood formation disorders. Compounds identified
 CC as binding to the proteins are used for the treatment of such disorders.
 XX
 SQ Sequence 16 BP; 3 A; 0 C; 8 G; 5 T; 0 other;

Query Match 92.0%; Score 13.8; DB 21; Length 16;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCTCCA 15
 :||||:|||||
 Db 16 ACTCCACTCACTCCA 2

RESULT 9
 AAV27168
 ID AAV27168 standard; DNA; 18 BP.

XX AC AAV27168;

XX DT 29-SEP-1998 (first entry)

XX DE Haemopoietin receptor primer 2057.

XX KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;

```
AC AA290848;
XX
XX 24-MAY-2000 (first entry)
XX
DE Human NR8 gene probe #76.
XX
XX Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX
XX Homo sapiens.
XX
XX WO9967290-A1.
XX
XX 29-DEC-1999.
XX
XX 23-JUN-1999; 99WO-JP03351.
XX
XX 24-JUN-1998; 98JP-0214720.
XX
XX 19-OCT-1998; 98JP-0297409.
XX
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
XX Nomura H, Maeda M;
XX
XX WPI; 2000-116933/10.
XX
XX Haemopoietin receptor protein family NR8 used for diagnosis of blood
XX formation disorders -
XX
XX Example 1; Page 41; 176pp; Japanese.
XX
XX The invention relates to the isolation of sequences encoding human
XX haemopoietin receptor protein family NR8 genes. The NR8 family
XX sequences were initially searched for comparison on a nucleic acid
XX database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
XX the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
XX AA259258-259300 and AA290816-290925 represent specific examples of probe
XX sequences used in the search. Antibodies to the NR8 family proteins are
XX used for the diagnosis of blood formation disorders. Compounds identified
XX as binding to the proteins are used for the treatment of such disorders.
XX
XX Sequence 15 BP; 4 A; 0 C; 7 G; 4 T; 0 other;

Query Match 92.0%; Score 13.8; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. NO. 1.4e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCCTCCA 15
   :|||||:|||||
Db 15 ACTCCATTCACTCCA 1

RESULT 5
AAZ90864/C
ID AAZ90864 standard; DNA; 15 BP.
XX
XX AC AAZ90864;
XX
XX 24-MAY-2000 (first entry)
XX
XX Human NR8 gene probe #92.
XX
XX Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX
XX Homo sapiens.
XX
XX WO9967290-A1.
XX
XX 29-DEC-1999.
XX
XX 23-JUN-1999; 99WO-JP03351.
XX
XX The invention relates to the isolation of sequences encoding human
XX haemopoietin receptor protein family NR8 genes. The NR8 family
XX sequences were initially searched for comparison on a nucleic acid
XX database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
XX the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
XX AA259258-259300 and AA290816-290925 represent specific examples of probe
XX sequences used in the search. Antibodies to the NR8 family proteins are
XX used for the diagnosis of blood formation disorders. Compounds identified
XX as binding to the proteins are used for the treatment of such disorders.
XX
XX Sequence 15 BP; 4 A; 0 C; 7 G; 4 T; 0 other;
```

```
XX
XX 24-JUN-1998; 98JP-0214720.
XX
XX 19-OCT-1998; 98JP-0297409.
XX
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
XX Nomura H, Maeda M;
XX
XX WPI; 2000-116933/10.
XX
XX Haemopoietin receptor protein family NR8 used for diagnosis of blood
XX formation disorders -
XX
XX Example 1; Page 42; 176pp; Japanese.
XX
XX The invention relates to the isolation of sequences encoding human
XX haemopoietin receptor protein family NR8 genes. The NR8 family
XX sequences were initially searched for comparison on a nucleic acid
XX database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
XX the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
XX AA259258-259300 and AA290816-290925 represent specific examples of probe
XX sequences used in the search. Antibodies to the NR8 family proteins are
XX used for the diagnosis of blood formation disorders. Compounds identified
XX as binding to the proteins are used for the treatment of such disorders.
XX
XX Sequence 15 BP; 3 A; 1 C; 8 G; 3 T; 0 other;

Query Match 92.0%; Score 13.8; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. NO. 1.4e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTCRCCTCCA 15
   :|||||:|||||
Db 15 GCTCCACTCACTCCA 1

RESULT 6
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ID AAZ90880 standard; DNA; 15 BP.
XX
XX AC AAZ90880;
XX
XX 24-MAY-2000 (first entry)
XX
XX Human NR8 gene probe #108.
XX
XX Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX
XX Homo sapiens.
XX
XX WO9967290-A1.
XX
XX 29-DEC-1999.
XX
XX 23-JUN-1999; 99WO-JP03351.
XX
XX 24-JUN-1998; 98JP-0214720.
XX
XX 19-OCT-1998; 98JP-0297409.
XX
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
XX Nomura H, Maeda M;
XX
XX WPI; 2000-116933/10.
XX
XX Haemopoietin receptor protein family NR8 used for diagnosis of blood
XX formation disorders -
XX
XX Example 1; Page 43; 176pp; Japanese.
XX
XX The invention relates to the isolation of sequences encoding human
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2

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 18:12:59 ; Search time 301.32 Seconds
(without alignments)
31.258 Million cell updates/sec

Title: US-09-532-263-6

Perfect score: 15

Sequence: 1 RCTCCAYTCRTCCA 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.8	92.0	15	AAT17870	Haemopoietin recep
2	13.8	92.0	15	AAV27139	Novel haemopoietin
3	13.8	92.0	15	AAZ90830	Human NR8 gene pro
4	13.8	92.0	15	AAZ90848	Human NR8 gene pro
5	13.8	92.0	15	AAZ90864	Human NR8 gene pro
6	13.8	92.0	15	AAZ90880	Human NR8 gene pro
7	13.8	92.0	15	AAZ90893	Human NR8 gene pro
8	13.8	92.0	16	AAZ90894	Human NR8 gene pro
9	13.8	92.0	18	AAV27168	Haemopoietin recep
10	13.8	92.0	21	AAF95960	Human gene single
11	13.8	92.0	25	AAT96787	Human and macaque

C 12	13.8	92.0	71	21	AAAG1554	Human IL-5R alpha
C 13	13.8	92.0	330	21	AAZ59255	Fragment of mouse
C 14	13.8	92.0	444	21	AAAG9731	Mouse IL-3 recepto
C 15	13.8	92.0	465	19	AAV22698	Interleukin-13 bin
C 16	13.8	92.0	657	21	AAZ94555	Cytokine receptor
C 17	13.8	92.0	690	16	AAT04952	Interleukin 4 comp
C 18	13.8	92.0	693	15	AAO54831	IL-2 receptor gamm
C 19	13.8	92.0	696	18	AAV04437	Interleukin 4 rece
C 20	13.8	92.0	759	15	AAQ54830	IL-2 receptor gamm
C 21	13.8	92.0	807	10	AAAN90793	Clone cm2-8 encodi
C 22	13.8	92.0	870	21	AAZ50746	HUMAN Orphan Cytok
C 23	13.8	92.0	907	21	AAZ59253	Human NR8gamma 3'
C 24	13.8	92.0	931	21	AAF20982	Human low adenosin
C 25	13.8	92.0	931	21	AAAG34860	Human adenosine re
C 26	13.8	92.0	938	19	AAV27142	Novel haemopoietin
C 27	13.8	92.0	938	21	AAA45793	DNA encoding a mur
C 28	13.8	92.0	947	19	AAV22702	Mature interleukin
C 29	13.8	92.0	975	21	AAA70701	Human interleukin
C 30	13.8	92.0	1035	21	AAZ40288	SR345 coding seque
C 31	13.8	92.0	1044	15	AAQ54829	IL-2 receptor gamm
C 32	13.8	92.0	1074	18	AAV04440	Interleukin 6 rece
C 33	13.8	92.0	1079	19	AAV22701	Construct containi
C 34	13.8	92.0	1126	18	AAT96784	Celebus macaque zc
C 35	13.8	92.0	1128	21	AAZ59247	Human NR8alpha/TPO
C 36	13.8	92.0	1167	18	AAT96783	Human Zytot2 cyto
C 37	13.8	92.0	1188	13	AAQ22974	Sequence of the op
C 38	13.8	92.0	1218	20	AAZ06347	Nucleotide sequenc
C 39	13.8	92.0	1218	21	AAZ50346	Mouse orphan cyto
C 40	13.8	92.0	1229	21	AAZ94577	Mouse cytokine rec
C 41	13.8	92.0	1233	20	AAZ08861	Human DNAX soluble
C 42	13.8	92.0	1260	13	AAQ22972	Sequence encoding
C 43	13.8	92.0	1260	20	AAZ09202	Human IL-6 recepto
C 44	13.8	92.0	1281	20	AAZ89654	cDNA encoding a hu
C 45	13.8	92.0	1288	19	AAV04131	Human HR-1 recepto

ALIGNMENTS

RESULT 1
AAT17870
ID AAT17870 standard; DNA; 15 BP.
XX AAT17870;
AC AAT17870;
XX 21-MAY-1996 (first entry)
DT Haemopoietin receptor probe HVB1.
XX Haemopoietin receptor probe HVB1.

XX Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
therapy; diagnosis; probe; hybridisation; ss.

OS Synthetic.

XX WO9607737-A1.

XX 14-MAR-1996.

PD 05-SEP-1995; 95WO-AU00578.

XX 05-SEP-1994; 94AU-0007902.

PR 05-SEP-1994; 94AU-0007901.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

PA Hilton DJ;

XX WPI; 1996-171612/17.

XX Nucleic acid encoding haemopoietin receptor containing conserved
PT amino acid motif esp. IL-11 receptor alpha chain - used for
PT developing IL-11 (ant)agonists

Search completed: August 29, 2001, 19:51:58
Job time: 17236 sec

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Best Local Similarity	80.0%; Pred. No. 8.6e+02;				
Matches 12; Conservative	3; Mismatches 0; Indels 0; Gaps 0;				
QY	1 RCTCCARTCRCTCCA 15 : :				
Db	669 ACTCCAGTCACTCCA 655				
RESULT 15					
AF329103/c					
LOCUS	AF329103 1227 bp DNA PLN 29-JAN-2001				
DEFINITION	Stachybotrys chartarum trichodiene synthase (TRI5) gene, complete cds.				
ACCESSION	AF329103				
VERSION	AF329103.1 GI:12584944				
KEYWORDS	Stachybotrys chartarum.				
SOURCE	Stachybotrys chartarum.				
ORGANISM	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.				
REFERENCE	1 (bases 1 to 1227)				
AUTHORS	Peplow A.W. and Beremand, M.N.				
TITLE	Putative trichothecene genes of Stachybotrys chartarum				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1227)				
AUTHORS	Peplow A.W. and Beremand, M.N.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-DEC-2000) Department of Plant Pathology & Microbiology, Texas A&M University, 2132 TAMUS, College Station, TX 77843-2132, USA				
FEATURES	Location/Qualifiers				
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	Join(<1..469,545..>1227)				
	/gene="TRI5"				
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	/translation="MEAFPTFVFLGTAVRLLENVYRDSNYTREERVENLQYAYNKA AHFAFQQOILKVSPPKRLASLRTIVGVVYSWAKVSKELMADLSIHYYTLILDFFG EDDPHMLTYFDLQSGNPQKHPWMLVNEHFPNVLRFHGPFCNLIRSLTLDFFG CWIEQYNHFGPSPFDYPCFLRMNGLCHVCGSLWPKENFNEQEHLEITSAIAQME NMMVWNLMSFYKEDDPDRTSLVKNYVSEGITLQALEKLQDTLQSSQEMMYV FSQOKPDLITCEPMHGVIYTHLDCNRYRLKEIYDRTDIQTEDAMKFRKFEQAQF VGAIEATWATYPTVVERLEQRKAERDEQAALNPEKAQVAVLA"				
BASE COUNT	321 a	326 c	316 g	264 t	
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Best Local Similarity	80.0%; Pred. No. 8.6e+02;				
Matches 12; Conservative	3; Mismatches 0; Indels 0; Gaps 0;				
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Db	1135 GCTCCATCGCTCCA 1121				

8-10, complete cds.
L38025
VERSION L38025.1 GI:608654
KEYWORDS ciliary neurotrophic factor alpha receptor.
SEGMENT 6 of 6
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 993)
AUTHORS Valenzuela, D.M., Rojas, E., Le Beau, M.M., Espinosa, R., Brannan, C.I.,
McClain, J., Masiakowski, P., Ip, N.Y., Copeland, N.G., Jenkins, N.A.
and Yancopoulos, G.D.
TITLE Genomic organization and chromosomal localization of the human and
mouse genes encoding the alpha receptor component for ciliary
neurotrophic factor
JOURNAL Genomics 25 (1), 157-163 (1995)
MEDLINE 95293367
FEATURES
Source 1..993
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Best Local Similarity 80.0%; Pred. No. 8.5e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 139 GCTCCAGTCACTCCA 125
standard; RNA; HUM; 999 BP.

RESULT 12
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ID E11420
XX
AC E11420;
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SV E11420.1
XX
DT 08-OCT-1997 (Rel. 52, Created)
DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX

cDNA encoding Ig-CRH region of human G-CSF receptor.
JP 1996140678-A/2.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN 1-999
RA Ota Y., Hirakawa O., Anaguchi H.;
RT "DNA CODING FOR PROTEIN OF LIGAND-BONDING REGION CONTAINING CRH REGION OF
GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR";
RL Patent number JP1996140678-A/2, 04-JUN-1996.
RL TANPAKU KOGAKU KENKYUSHO:KK.
XX
CC OS Homo sapiens (human)
CC PN JP 1996140678-A/2
CC PD 04-JUN-1996
CC PF 15-NOV-1994 JP 1994280655
CC PI Ota YOSHIMI, HIRAKAWA OSAMU, ANAGUCHI HIROYUKI
CC PC C12N15/09,C07H21/04,C07K14/715,C12N5/10,C12P21/02,(C12N5/10,
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CC CC topology: Linear;
CC CC hypothetical: No;
CC CC anti-sense: No;
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LOCUS GGU29245 1089 bp mRNA VRT 16-FEB-1996
DEFINITION Gallus gallus ciliary neurotrophic factor receptor alpha component
mRNA, complete cds.
ACCESSION U29245
VERSION U29245.1 GI:1151068
KEYWORDS chicken.
SOURCE Gallus gallus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1089)
AUTHORS Ip, F.C., Fu, A.K., Tsui, K.W. and Ip, N.Y.
TITLE Cloning of the alpha component of the chick ciliary neurotrophic
factor receptor: developmental expression and down-regulation in

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XX FH Key Location/Qualifiers
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Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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XX SV EL1371.1
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XX DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
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XX KW JP 1996131172-A/2.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
XX [1]
XX RA Ota Y., Anaguchi H.;
XX RT "DNA CODING PROTEIN BC IN LIGAND-BOUND REGION IN GRANULOCYTE COLONY
XX RT STIMULATING FACTOR RECEPTOR";
XX RL Patent number JP1996131172-A/2, 28-MAY-1996.
XX RL TANPAKU KOGAKU KENKYUSHO:KK.
XX OS Homo sapiens (human)
XX PN JP 1996131172-A/2
XX PD 28-MAY-1996
XX PF 14-NOV-1994 JP 1994278841
XX PC OTA YOSHIMI, ANAGUCHI HIROYUKI
XX PC C12N15/09, C07H21/04, C07K14/715, C12N1/21, C12P21/02, (C12N1/21,
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XX CC hypothetical: NO;
XX CC anti-sense: No;
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Query Match 92.0%; Score 13.8; DB 45; Length 639;
Best Local Similarity 80.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
Db 606 GTCCAGTCGCTCCA 592

RESULT 10
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LOCUS MUMULEPR06 801 bp DNA ROD 09-JAN-1998
DEFINITION Mus musculus leptin receptor (Lepr) gene, exon 6.
ACCESSION AF039448
VERSION AF039448.1 GI:2760934
KEYWORDS 6 of 19
SEGMENT house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 801)
REFERENCE Chua, S.C., Chung, W.K., Wu-Peng, X.S., Zhang, Y., Liu, S.M.,
AUTHORS Tartaglia, L., and Leibel, R.L.
Phenotypes of mouse diabetes and rat fatty due to mutations in the
OB (leptin) receptor
JOURNAL Science 271 (5251), 994-996 (1996)
MEDLINE 96172360
AUTHORS 2 (bases 1 to 801)
REFERENCE Chua, S.C., Kouttras, I.K., Han, L., Liu, S.M., Kay, J., Young, S.J.,
Chung, W.K., and Leibel, R.L.
TITLE Fine structure of the murine leptin receptor gene: splice site
suppression is required to form two alternatively spliced
transcripts
JOURNAL Genomics 45 (2), 264-270 (1997)
MEDLINE 98008913
REFERENCE 3 (bases 1 to 801)
AUTHORS Chua, S.C., Kouttras, I.K., Han, L., Liu, S.M., Kay, J., Young, S.J.,
Chung, W.K., and Leibel, R.L.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-1997) Pediatrics, Columbia University, 1150 St.
Nicholas Avenue, New York, NY 10032, USA
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/chromosome="4"
300..444
/gene="Lepr"
/number=6
BASE COUNT 188 a 143 c 199 g 270 t 1 others
ORIGIN

Query Match 92.0%; Score 13.8; DB 94; Length 801;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
Db 419 ACTCCAGTCACCTCCA 405

RESULT 11
HUMCNFR06/c
LOCUS HUMCNFR06 993 bp DNA PRI 09-JAN-2001
DEFINITION Homo sapiens ciliary neurotrophic factor alpha receptor gene, exons

```

```

MEDLINE      97224611
REFERENCE    2 (bases 1 to 597)
AUTHORS      Coleman,A.W. and Mai,J.C.
TITLE        Direct Submission
JOURNAL      Submitted (15-AUG-1996) Biomed, Brown University, Providence, RI
              02912, USA
COMMENT      On Nov 20, 1997 this sequence version replaced gi:2039187.
FEATURES
  source      Location/Qualifiers
              1..597
              /organism="Chlamydomonas incerta"
              /strain="SAG7.73"
              /db_xref="taxon:51695"
              1..199
              /note="ITS1"
              /product="internal transcribed spacer 1"
              200..358
              /product="5.8S ribosomal RNA"
              359..597
              /note="ITS2"
              /product="internal transcribed spacer 2"
BASE COUNT   157 a 156 c 142 g 142 t
ORIGIN
Query Match.          92.0%; Score 13.8; DB 14; Length 597;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCARTCRCTCCA 15
   :||||:|||||
Db 399 GCTCCAATCACTCCA 385

RESULT 7
G56634/c
LOCUS        G56634      620 bp      DNA           STS           30-MAR-2000
DEFINITION   SHGC-102031 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION    G56634
VERSION      G56634.1 GI:6121803
KEYWORDS     STS.
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 620)
AUTHORS      Olivier,M. and Cox,D.R.
TITLE        Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL      Unpublished (2000)
COMMENT      Contact: Michael Olivier, David R. Cox
              Stanford Human Genome Center
              Stanford University School of Medicine
              4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
              Tel: (650) 320-5800
              Fax: (650) 320-5801
              Email: olivier@shgc.stanford.edu
              Primer A: TTTCCTGCTGTCCTTGTCCTCAAT
              Primer B: GATTCATCAGGTCGACGCAATTC
              STS size: 281
              PCR Profile:
                  Initial incubation: 95 degrees C for 10 minutes
                  Denaturation: 94 degrees C for 30 seconds
                  Annealing: 60 degrees C for 30 seconds
                  Polymerization: 72 degrees C for 23 seconds
                  PCR Cycles: 30
                  Thermal Cycler: Perkin Elmer 9700
              Protocol:
                  Template: 25 ng
                  Primer: each 1 uM
                  dNTPs: each 200 uM
                  Amplitaq Gold Polymerase: 0.07 units/ul
                  Total Vol: 5 ul

```

```

Buffer:      MgCl2:      2.5 mM
              KCl:       50 mM
              Tris-HCl:   10 mM
              pH:         8.3

BAC ends sequenced at TIGR from the RPC111 BAC library. Designed
and developed at the Stanford Human Genome Center.

FEATURES
  source      Location/Qualifiers
              1..620
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /map="11"
              /clone_lib="Human"
              STS
              primer_bind 267..547
              primer_bind complement(525..547)
BASE COUNT   157 a 123 c 147 g 193 t
ORIGIN
Query Match.          92.0%; Score 13.8; DB 54; Length 620;
Best Local Similarity 80.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCARTCRCTCCA 15
   :||||:|||||
Db 151 GCTCCAATCACTCCA 137

RESULT 8
E09857/c
ID E09857 standard; RNA; HUM; 639 BP.
XX
AC E09857;
XX
SV E09857.1
XX
DT 08-OCT-1997 (Rel. 52, Created)
DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX
DE cDNA encoding CRH region of G-CSF receptor.
XX
KW JP 1995227288-A/2.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-639
RA Ota Y., Anaguchi H., Hiraoka O.;
RT "DNA CODING FOR LIGAND BIND RANGE PROTEIN OF GRANULOCYTE COLONY STIMULATION
RT FACTOR RECEPTOR";
RL Patent number JP1995227288-A/2, 29-AUG-1995.
XX
OS Homo sapiens (human)
CC PN JP 1995227288-A/2
CC PD 29-AUG-1995
CC PF 30-MAY-1994 JP 1994116252
CC PR 21-DEC-1993 JP 93P 321862
CC PI Ota YOSHIMI, ANAGUCHI HIROYUKI, HIRAOKA OSAMU
CC PC C12N15/09,C12P21/02,(C12N15/09,C12R1:91),(C12P21/02,C12R1:19);
CC CC strandedness: Double;
CC CC topology: Linear;
CC CC hypothetical: No;
CC CC anti-sense: No;
CC CC Key
CC FH Location/Qualifiers
CC FT 1..639
CC FT /organism="Homo sapiens"
CC FT /tissue_type="Placenta"

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9699267
PUBMED
REFERENCE 3 (bases 1 to 373)
AUTHORS van der Poel,J.J.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-1997) Animal Breeding, Agricultural University Wageningen, Marijkeweg 40, Wageningen 6708 PG, The Netherlands
COMMENT GSDS:S:48171.
[Flatfile retrieved from GSDS Fri Feb 23 09:21:05 2001].

FEATURES
source
1..373
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="CDNA42R"
/tissue_type="brain"
/dev_stage="adult"
/note="derived from cDNA library".
repeat_region
1..373
/note="microsatellite MCW111"
/rpt_type=tandem
BASE COUNT 140 a 74 c 53 g 102 t 4 others
ORIGIN
1 RTCCARTCRCTCCA 15
:||||:|||||
Db 307 ACTCCAATCACTCCA 321

Query Match 92.0%; Score 13.8; DB 8; Length 373;
Best Local Similarity 80.0%; Pred. No. 8e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTCCARTCRCTCCA 15
LOCUS :||||:|||||
Db 307 ACTCCAATCACTCCA 321

RESULT 4
S4713456/c
LOCUS
DEFINITION unc-5-immunoglobulin and thrombospondin type 1 transmembrane protein [alternatively spliced] [Caenorhabditis elegans, variety Bergerac, Genomic/mRNA, 387 nt, segment 6 of 9].
ACCESSION S47165
VERSION S47165.1 GI:258524
KEYWORDS
SEGMENT
SOURCE
ORGANISM Caenorhabditis elegans variety Bergerac.
REFERENCE 1 (bases 1 to 387)
AUTHORS Leung-Hagsteel,J.N., Spence,A.M., Stern,B.D., Zhou,Y., Su,M.W., Hedgecock,E.M. and Culotti,J.G.
TITLE UNC-5, a transmembrane protein with immunoglobulin and thrombospondin type 1 domains, guides cell and pioneer axon migrations in C. elegans
JOURNAL Cell 71 (2), 289-299 (1992)
MEDLINE 93046629
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 116678] from the original journal article.
This sequence comes from Fig. 2.

FEATURES
source
1..387
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/variety="Bergerac"
BASE COUNT 106 a 84 c 107 g 90 t
ORIGIN
1 RTCCARTCRCTCCA 15
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QY 1 RTCCARTCRCTCCA 15
LOCUS :||||:|||||
Db 261 ACTCCAATCACTCCA 247

Query Match 92.0%; Score 13.8; DB 96; Length 387;
Best Local Similarity 80.0%; Pred. No. 8e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTCCARTCRCTCCA 15
LOCUS :||||:|||||
Db 261 ACTCCAATCACTCCA 247

RESULT 5
AF227555/c
LOCUS
DEFINITION Macaca mulatta interleukin-6 signal transducer receptor (IL-6) mRNA, partial cds.
ACCESSION AF227555
VERSION AF227555.1 GI:8132802
KEYWORDS
SOURCE rhesus monkey.
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 457)
AUTHORS Arredondo,J.
TITLE Cytokine Signal Transduction Genes from Rhesus Macaques
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 457)
AUTHORS Arredondo,J.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-2000) California Regional Primate Research Center, University of California-Davis, One Shields Avenue, Davis, CA 95616, USA
FEATURES
source
1..457
/organism="Macaca mulatta"
/db_xref="taxon:9544"
/cell_type="peripheral blood mononuclear cells"
<1..>457
/gene="IL-6"
/note="gp130"
<1..>457
/gene="IL-6"
/note="membrane glycoprotein"
/codon_start=2
/product="interleukin-6 signal transducer receptor"
/protein_id="AA073398.1"
/db_xref="GI:8132803"
/translation="PAEDTASTRSSTVQDLKPFTEYVFRICCKEDGKGYMSWSEE
ANGTYEDRPSKPSFWYKIDPSHAQGYRTVQLMKTKLPPEANGKIDYEVTLTRWK
SHLQNTVNDTKLTNLTNDRYVATLTARNLVGKSDAAVLTPACDFQT"
BASE COUNT 155 a 93 c 88 g 121 t
ORIGIN
1 RTCCARTCRCTCCA 15
:||||:|||||
Db 127 ACTCCAATCACTCCA 113

Query Match 92.0%; Score 13.8; DB 89; Length 457;
Best Local Similarity 80.0%; Pred. No. 8.1e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTCCARTCRCTCCA 15
LOCUS :||||:|||||
Db 127 ACTCCAATCACTCCA 113

RESULT 6
CIU66950/c
LOCUS
DEFINITION Chlamydomonas incerta internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.
ACCESSION U66950
VERSION U66950.1 GI:2627277
KEYWORDS
SOURCE Chlamydomonas incerta.
ORGANISM Chlamydomonas incerta
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
REFERENCE 1 (bases 1 to 597)
AUTHORS Mai,J.C. and Coleman,A.W.
TITLE The internal transcribed spacer 2 exhibits a common secondary structure in green algae and flowering plants
JOURNAL J. Mol. Evol. 44 (3), 258-271 (1997)

```

c 9 13.8 92.0 639 45 E11371 cDNA encodi
c 10 13.8 92.0 801 94 HUMOLEPRO6
c 11 13.8 92.0 993 97 HUMCNFAR06
c 12 13.8 92.0 999 45 E11420
c 13 13.8 92.0 1089 45 GGU29245
c 14 13.8 92.0 1218 91 HLPRI108
c 15 13.8 92.0 1227 13 AF329103
c 16 13.8 92.0 1248 8 GGGPARA
c 17 13.8 92.0 1332 95 S54212
c 18 13.8 92.0 1423 5 AF133269
c 19 13.8 92.0 1514 12 AF053926
c 20 13.8 92.0 1566 97 HUMCNTER
c 21 13.8 92.0 1591 9 AR066232
c 22 13.8 92.0 1591 9 AR070290
c 23 13.8 92.0 1591 9 AR074863
c 24 13.8 92.0 1591 10 I12552
c 25 13.8 92.0 1591 10 I56052
c 26 13.8 92.0 1593 7 OC090928
c 27 13.8 92.0 1680 95 S80963
c 28 13.8 92.0 1707 10 I50845
c 29 13.8 92.0 1878 85 AB015706
c 30 13.8 92.0 1975 94 AF068615
c 31 13.8 92.0 1977 9 A49472
c 32 13.8 92.0 1977 9 AR079661
c 33 13.8 92.0 2272 8 AF041846
c 34 13.8 92.0 2369 9 AR019619
c 35 13.8 92.0 2369 9 AR070271
c 36 13.8 92.0 2416 94 AB012290
c 37 13.8 92.0 2418 94 MM049110
c 38 13.8 92.0 2460 94 BC005707
c 39 13.8 92.0 2466 5 AF135119
c 40 13.8 92.0 2469 94 MM041115
c 41 13.8 92.0 2502 94 MUSSDFLIFR
c 42 13.8 92.0 2546 93 HSGCSFRD
c 43 13.8 92.0 2547 7 AF167719
c 44 13.8 92.0 2644 7 BTA308426
c 45 13.8 92.0 2647 89 AK022852

```

ALIGNMENTS

```

RESULT 1
A70377 A70377 15 bp DNA PAT 07-MAY-1999
LOCUS Sequence 7 from Patent WO9811225.
DEFINITION A70377
ACCESSION A70377
VERSION A70377.1 GI:4774658
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., HilCon,D.J., Kojima,T., Maeda,M. and
Kikuchi,I.
TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL Patent: WO 9811225-A 7 19-MAR-1998;
NICOLO NICOS ANTONY (AU)
FEATURES
Source Location/Qualifiers
2 a 7 c 3 others
BASE COUNT 2 a 7 c 3 others
ORIGIN
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Query Match 92.0%; Score 13.8; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RCTCCARTCRCTCCA 15
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Db 1 RCTCCARTCRCTCCA 15
RESULT 2
HSJ10F12/c
LOCUS HSJ10F12 340 bp DNA STS 07-MAR-2000
DEFINITION STS from H.sapiens random shear fragment, sequence tagged site.
ACCESSION AL159451
VERSION AL159451.1 GI:7210385
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 340)
AUTHORS Hunt,S., Sims,S., Willey,D., Carter,N. and Ross,M.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2000) E-mail contact: humquery@sanger.ac.uk
COMMENT Marker sts67529 (primer A : AAAAGTGAAGAGGGAAGG; primer B :
GATAACCAAGCGCATGG; amplicon size : 141 bp) was developed from a
single pass sequencing read from H.sapiens flow-sorted chromosome
9-12 random shear fragment, SC9-12p10F12. Vector : pUC18 Site :
SmaI
Further information : http://www.sanger.ac.uk/HGP/Chr10/.
FEATURES
Source Location/Qualifiers
1..340
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/sex="male"
/clone="SC9-12p10F12"
/tissue_type="Lymphoblastoid cell line"
/clone_lib="SC9-12p1"
BASE COUNT 131 a 44 c 77 g 87 t 1 others
ORIGIN
Query Match 92.0%; Score 13.8; DB 54; Length 340;
Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 RCTCCARTCRCTCCA 15
|||||
Db 48 GTCCTCAGTCACTCCA 34
RESULT 3
L48909 L48909 373 bp mRNA VRT 23-FEB-2001
LOCUS Gallus gallus clone cDNA42R microsatellite MCW111 sequence.
DEFINITION L48909
ACCESSION L48909
VERSION L48909.1 GI:13111695
KEYWORDS
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 373)
AUTHORS Ruyter-Spira,C.P., Crooijmans,R.P., Dijkhof,R.J., van Oers,P.A.,
Strijk,J.A., van der Poel,J.J. and Groenen,M.A.
TITLE Development and mapping of polymorphic microsatellite markers
derived from a chicken brain cDNA library
JOURNAL Anim. Genet. 27 (4), 229-234 (1996)
MEDLINE 97009815
PUBMED 8856919
REFERENCE 2 (bases 1 to 373)
AUTHORS Ruyter-Spira,C.P., de Koning,D.J., van der Poel,J.J.,
Crooijmans,R.P., Dijkhof,R.J. and Groenen,M.A.
TITLE Developing microsatellite markers from cDNA: a tool for adding
expressed sequence tags to the genetic linkage map of the chicken
JOURNAL Anim. Genet. 29 (2), 85-90 (1998)
MEDLINE 98364423

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:51:55 ; Search time 1774.1 Seconds
(without alignments)
130.780 Million cell updates/sec

Title: US-09-532-263-7
Perfect score: 15
Sequence: 1 RCTCCARTCRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ba3:*
- 4: gb_in1:*
- 5: gb_in2:*
- 6: gb_in3:*
- 7: gb_om:*
- 8: gb_ov:*
- 9: gb_pat1:*
- 10: gb_pat2:*
- 11: gb_ph:*
- 12: gb_pl1:*
- 13: gb_pl2:*
- 14: gb_pl3:*
- 15: gb_pl4:*
- 16: em_ba1:*
- 17: em_ba2:*
- 18: em_fun:*
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- 20: em_htgo_inv:*
- 21: em_htgo_rod:*
- 22: em_htg_hum1:*
- 23: em_htg_hum2:*
- 24: em_htg_hum3:*
- 25: em_htg_hum4:*
- 26: em_htg_hum5:*
- 27: em_htg_hum6:*
- 28: em_htg_hum7:*
- 29: em_htg_hum8:*
- 30: em_htg_inv1:*
- 31: em_htg_inv2:*
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- 91: gb_pr7:*
- 92: gb_pr8:*
- 93: gb_pr9:*
- 94: gb_ro1:*
- 95: gb_ro2:*
- 96: gb_in4:*
- 97: gb_pr10:*
- 98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	13.8	92.0	15	9 A70377	A70377 Sequence 7
C 2	13.8	92.0	340	54 HSJ10F12	AL159451 STS from
3	13.8	92.0	373	8 L48909	L48909 Gallus gall
C 4	13.8	92.0	387	96 S47134S6	S47165 unc-5-immun
C 5	13.8	92.0	457	89 AF227555	AF227555 Macaca mu
C 6	13.8	92.0	597	14 CIU66950	U66950 Chlamydomon
C 7	13.8	92.0	620	54 G56634	G56634 SHGC-102031
C 8	13.8	92.0	639	45 E09857	E09857 cDNA encodi

XX 27-MAR-1998; 98WO-US06056.
 XX
 XX 28-MAR-1997; 97US-0042849.
 XX
 XX (CYTO-) CYTOCLONAL PHARM INC.
 XX
 XX Labidi AH;
 PI
 XX
 XX WPI; 1998-568277/48.
 DR
 XX
 XX Recombinant non-pathogenic Mycobacterium as vaccines providing long
 PT term cellular immunity - useful against intracellular pathogens,
 PT cancer and autoimmune disease, and are retained in host macrophages
 XX
 XX Disclosure; Fig 6; 120pp; English.
 PS
 XX This genomic DNA sequence is a fragment of the Mycobacterium fortuitum
 CC plasmid PAL 5000 which contains ORF2. This sequence is used in a
 CC method which results in the formation of Mycobacterium recombinant
 CC vaccines from compositions that provide a continuous source of protein to
 CC an animal and stimulate cellular immunity. Such compositions are used to
 CC stimulate cellular immunity (by inducing Th-1 cells or cytotoxic T
 CC lymphocytes), particularly as vaccines (live or dead) for treating and
 CC preventing diseases caused by intracellular pathogens (bacteria, viruses,
 CC rickettsia or protozoa), and also cancer, autoimmune diseases, allergy
 CC and bovine spongiform encephalitis, in humans or animals. The vaccines
 CC are administered by injection, orally and nasally. These compositions
 CC provide consistent and long-lasting immunity. Transformed cells used in
 CC the method are retained within macrophages, blocking the killing
 CC mechanism but producing protective immunogen which is processed and
 CC presented by the macrophage. Several immunogens may be included in the
 CC same vaccine and the Mycobacterium cells serve as adjuvant.
 XX
 SQ Sequence 2096 BP; 348 A; 743 C; 670 G; 335 T; 0 other;

Query Match 92.0%; Score 13.8; DB 19; Length 2096;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCTCCARTCRCTCCA 15
 Db 1481 gctccaatgctcca 1495

Search completed: August 29, 2001, 20:16:42
 Job time: 7423 sec

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCARTCRCTCCA 15
:|||||:|||||
Db 1170 GCTCCAGTCACTCCA 1156

RESULT 13
AAQ83223/C
ID AAQ83223 standard; cDNA; 1591 BP.

XX AC AAQ83223;

XX DT 22-SEP-1995 (first entry)

XX DE Human recombinant mature CNTFR.

XX KW CNTFR; ciliary neurotrophic factor receptor; cytokine;

XX KW agonist; antagonist; signal transduction pathway; PRPN151;

XX KW Escherichia coli; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 289..1407

XX FT /*tag= a

XX FT mat_peptide 289..1404

XX FT /*tag= b

XX PN WO9507467-A.

XX PD 16-MAR-1995.

XX PF 09-SEP-1994; 94WO-US10163.

XX PR 09-SEP-1993; 93US-0118968.

XX PA (REG-) REGENERON PHARM INC.

XX PA (SUUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX PI Ihle JN, Stahl N, Yancopoulos GD;

XX DR WPI; 1995-123515/16.

XX DR P-PSDB; AAR70147.

XX PT Detection of ciliary neurotrophic factor receptor agonists - by

XX PT determination of levels of phosphorylation.

XX PS Disclosure; Fig.2a-2d; 125pp; English.

XX CC The gene encoding human CNTFR was subcloned into bacterial

XX CC expression vector pC110. The resulting plasmid, PRPN151,

XX CC encoded a recombinant, mature form of human CNTFR. Further

XX CC manipulation of the coding region optimized expression of the

XX CC gene in E. coli RJ26, allowing production of useful amounts

XX CC of CNTFR.

XX SQ Sequence 1591 BP; 288 A; 538 C; 473 G; 292 T; 0 other;

Query Match 92.0%; Score 13.8; DB 16; Length 1591;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCARTCRCTCCA 15
:|||||:|||||
Db 1170 GCTCCAGTCACTCCA 1156

RESULT 14
AAT14602/C
ID AAT14602 standard; DNA; 1977 BP.
XX

AC AAT14602;

XX DT 20-JUN-1996 (first entry)

XX DE Human gp130 splice variant gene.

XX KW Gp130; transmembrane domain; growth factor antagonist;

XX KW embryo pre-implantation; in vitro fertilisation; ss.

XX OS Homo sapiens.

XX PN WO9609382-A1.

XX PD 28-MAR-1996.

XX PF 21-SEP-1995; 95WO-GB02243.

XX PR 21-SEP-1994; 94GB-0019021.

XX PA (ISTF) ARS APPLIED RES SYST HOLDING NV.

XX PI Dellow KA, Sharkey A, Smith SK;

XX DR WPI; 1996-188444/19.

XX DR P-PSDB; AAR94576.

XX PT New splice variant of gp130 lacking the trans-membrane domain -

XX PT useful as an antagonist for growth factors esp. for ensuring correct

XX PT development of pre-implantation embryos

XX PS Example 2; Fig 1; 33pp; English.

XX CC A DNA sequence (AAT14602) codes for a novel splice variant (AAR94576) of

XX CC human gp130. The splice variant was initially detected during the

XX CC morula to blastocyst transition stage of a human embryo. The

XX CC splicing event removes the exon coding for the transmembrane domain

XX CC causing a frameshift resulting in a novel C-terminus (see AAR94575).

XX CC The splice variant gp130 antagonises the action of certain growth

XX CC factors and can be used to ensure correct development of

XX CC preimplantation embryos, partic. for in vitro fertilisation.

XX SQ Sequence 1977 BP; 658 A; 396 C; 379 G; 544 T; 0 other;

Query Match 92.0%; Score 13.8; DB 17; Length 1977;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCARTCRCTCCA 15
:|||||:|||||
Db 942 ACTCCAGTCACTCCA 928

RESULT 15

AAV69318

ID AAV69318 standard; DNA; 2096 BP.

XX AC AAV69318;

XX DT 01-FEB-1999 (first entry)

XX DE M. fortuitum plasmid pAL 5000 genomic DNA fragment.

XX KW Vaccine; cellular immunity; Th-1 cell; cancer; cytotoxic T lymphocyte;

XX KW treatment; prevention; disease; autoimmune; intracellular pathogen; BSE;

XX KW allergy; bovine spongiform encephalitis; macrophage; immunogen;

XX KW adjuvant; ds.

XX OS Mycobacterium fortuitum.

XX PN WO9844096-A2.

XX PD 31-OCT-1998.

CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SQ Sequence 1419 BP; 333 A; 436 C; 384 G; 265 T; 1 other;

Query Match 92.0%; Score 13.8; DB 21; Length 1419;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
 :||||:|||||
 Db 545 gctccagtcactcca 559

RESULT 11
 AAQ20195/c
 ID AAQ20195 standard; cDNA; 1591 BP.
 XX AC AAQ20195;
 XX
 DT 31-MAR-1992 (first entry)
 XX
 DE Ciliary neurotrophic factor receptor-coding sequence.
 XX
 KW CNTFR; transgenic animal; motoneurone disease; trauma;
 KW muscular dystrophy; inflammation; amyotrophic lateral sclerosis; ds.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 CDS 289..1407
 FT /*tag= a
 FT /product= CNTFR

XX WO9119009-A.
 XX
 XX 12-DEC-1991.
 XX
 XX 03-JUN-1991; 91WO-US03896.
 XX
 XX 15-MAY-1991; 91US-0700677.
 XX 01-JUN-1990; 90US-0532285.
 XX 28-MAR-1991; 91US-0676647.
 XX
 XX (REGE-) REGENERON PHARM INC.
 XX
 XX Davis S, Squinto S, Furth M, Yancopoulos GD;
 XX WPI; 1992-007490/01.
 XX P-PSDB; AAR20024.

XX DNA encoding CNTF receptors - useful in diagnosis, physiological
 XX study and treatment of CNTF-related disorders
 XX
 XX Claim 2; Fig 2; 92pp; English.

XX The CNTFR coding sequence can be incorporated into cells, cell lines

CC and organisms (e.g. E.coli) for the expression of the receptor
 CC protein. Monoclonal antibodies can be raised to the CNTF. The cDNA
 CC can be used as a probe to screen a library for clones encoding
 CC members of the family of molecules including IL-6 receptor.
 XX
 SQ Sequence 1591 BP; 289 A; 545 C; 465 G; 292 T; 0 other;

Query Match 92.0%; Score 13.8; DB 13; Length 1591;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
 :||||:|||||
 Db 1170 GCTCCAGTCACCTCCA 1156

RESULT 12
 AAQ39626/c
 ID AAQ39626 standard; cDNA; 1591 BP.

XX AC AAQ39626;
 XX
 DT 30-SEP-1993 (first entry)
 XX

XX Sequence encoding human ciliary neurotrophic factor receptor (CNTF).
 XX
 KW Ciliary neurotrophic factor; receptor; protein complex; ds.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 CDS 289..1404
 FT /*tag= a

XX WO9311253-A.
 XX
 XX 10-JUN-1993.
 XX
 XX 01-DEC-1992; 92WO-US10632.
 XX
 XX 02-DEC-1991; 91US-0801562.
 XX 09-APR-1992; 92US-0865878.
 XX

XX (REGE-) REGENERON PHARM INC.
 XX
 XX Aldrich TH, Conover J, Davis S, Everdeen D, Ip N;
 XX Nye SH, Panayotatos N, Squinto SP, Stahl N, Yancopoulos GD;
 XX WPI; 1993-197070/24.
 XX P-PSDB; AAR37820.

XX Cell-free ciliary neurotrophic factor-receptor complex - for
 XX diagnosis and treatment of cell proliferation and differentiation
 XX disorders e.g. myeloid leukaemia
 XX
 XX Disclosure; Fig 2; 122pp; English.

XX CNTF has been cloned and synthesized in eukaryotic as well as
 XX bacterial expression systems, as described in International
 XX Application No. PCT/U.S. 90/05241. The CNTF receptor (CNTFR or CNTFR-
 XX alpha) has been cloned and expressed in eukaryotic cells, as
 XX described in U.S. Patent Application Serial No. 07/700,677 and
 XX International Application No. PCT/US91/03896, filed June 3, 1991.
 XX The present invention relates to a stable CNTF/receptor complex
 XX which possesses a different mobility in native polyacrylamide gels
 XX than either purified fractions of CNTF or CNTFR.

XX Sequence 1591 BP; 289 A; 536 C; 473 G; 293 T; 0 other;

Query Match 92.0%; Score 13.8; DB 14; Length 1591;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;

Query Match 92.0%; Score 13.8; DB 15; Length 1193;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
 :||||:|||||
 Db 824 ACTCCAGTCACTCCA 810

RESULT 9
 AAT66164/c
 ID AAT66164 standard; DNA; 1383 BP.
 XX
 AC AAT66164;
 XX
 DT 15-JUL-1997 (first entry)
 XX
 DE Mouse interleukin-12 receptor alpha chain NR4 DNA.
 XX
 KW NR4; haemopoietin receptor; interleukin-13 receptor; IL-13;
 KW cytokine; allergy; asthma; therapy; ss.
 XX
 OS Mus sp.

XX Key Location/Qualifiers
 FH CDS 61..1341
 FT /*tag= a
 FT sig_peptide 61..141
 FT /*tag= b
 FT mat_peptide 142..1338
 FT /*tag= c
 FT misc_difference 121..123
 FT /*tag= d
 FT /note= "bases 121-123 (nnn) code for an
 FT unidentified amino acid"
 FT misc_difference 640..642
 FT /*tag= e
 FT /note= "bases 640-642 (nnn) code for an
 FT unidentified amino acid"

XX WO9715663-A1.

PN 01-MAY-1997.
 XX
 PD 23-OCT-1996; 96WO-AU00668.
 XX
 PF 09-SEP-1996; 96AU-0002208.
 PR 23-OCT-1995; 95AU-0006135.
 PR 22-DEC-1995; 95AU-0007276.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Hilton DJ, Metcalf D, Nicola NA, Willson T, Zhang JG;
 XX
 XX WPI; 1997-259018/23.
 DR P-PSDB; AAW09821.

XX DNA encoding animal haemopoietin receptor which interacts with
 PT interleukin-13 - useful to treat asthma, allergy or condition
 PT exacerbated by IgE production

XX Claim 6; Page 48-50; 93pp; English.

XX DNA sequences (AAT66164 and AAT66165) respectively code for novel mouse
 CC and human haemopoietin receptors (AAW09821 and AAW09822) designated NR4
 CC that comprise the interleukin-13 (IL-13) receptor alpha-chain. To
 CC obtain the mouse sequence, genomic DNA prep. from embryonal stem
 CC cells was screened with oligonucleotides encoding an amino acid
 CC sequence (WSDWS) found in many haemopoietin receptors. The genomic
 CC clone was used to isolate NR4 cDNA clones from WEHI-231 cells,
 CC peritoneal macrophage, bone marrow, skin and kidney libraries, and
 CC a composite sequence for mouse NR4 was produced. The availability
 CC of genetic sequences for NR4 permits the development of a range of

CC agents capable of modulating the activity of IL-13 and related
 CC cytokines such as interleukin-4 for the treatment of allergy, asthma
 CC and other conditions relating to IgE. The genetic sequences can
 CC also be used in prodn. of recombinant NR4 or fusion proteins
 CC including NR4.

XX Sequence 1383 BP; 416 A; 296 C; 315 G; 350 T; 6 other;

Query Match 92.0%; Score 13.8; DB 18; Length 1383;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
 :||||:|||||
 Db 1050 ACTCCAGTCACTCCA 1036

RESULT 10
 AAC76452
 ID AAC76452 standard; cDNA; 1419 BP.

XX AC AAC76452;

XX 08-FEB-2001 (first entry)

XX Human ORFX ORF2007 polynucleotide sequence SEQ ID NO:4013.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.

XX Homo sapiens.

PN WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2000-602362/57.

XX P-PSDB; AAB42243.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

XX Claim 5; Page 3192-3193; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;

PA (KANF) KANEKA CORP.
 XX Kishimura M, Nakao K, Osakada F, Osaki S, Tanaka M;
 XX WPI; 1997-281030/25.
 DR P-PSDB; AAW17859.
 XX
 XX Auto-antigen from synovial cells of rheumatoid arthritis patients -
 PT binds to antibodies present in these patients, for diagnosis and
 PT prediction of the disease
 XX
 XX Claim 9; Page 38; 61pp; Japanese.
 XX
 XX The present sequence encodes the rheumatoid arthritis (RA)
 CC auto-antigen clone A, which can be used to diagnose and predict
 CC the development of RA by reaction with antibodies in biological
 CC specimens, e.g. sera, from patients.
 CC RNA was isolated from synovial cells from a RA patient and used to
 CC construct a cDNA library. This was screened using IgG separated
 CC from the synovial fluid of a RA patient. Active clones were
 CC isolated in a cloning vector, and inserted into an expression
 CC vector for the transformation of E. coli NM522. Transformsants on
 CC culture express clone A peptide and follistatin related protein
 CC into the culture medium.
 XX
 XX Sequence 990 BP; 321 A; 190 C; 193 G; 286 T; 0 other;
 SQ

Query Match 92.0%; Score 13.8; DB 18; Length 990;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
 :||||:|||||
 Db 942 ACTCCAGTCACTCCA 928

RESULT 7
 AAT35138/c
 ID AAT35138 standard; DNA; 999 BP.
 XX
 XX AAT35138;
 AC
 XX
 XX 30-OCT-1996 (first entry)
 DT
 XX
 XX DNA encoding cytokine-receptor-complementary region G-CSF receptor.
 DE
 XX
 XX G-CSF; granulocyte colony stimulating factor; receptor; leukaemia;
 KW over-proliferation; recombinant; vector; ds.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 1.999
 FT /*tag- a
 FT /note- "no stop codon"
 FT
 XX JP08140678-A.
 PN
 XX
 XX 04-JUN-1996.
 PD
 XX
 XX 15-NOV-1994; 94JP-0280655.
 PF
 XX
 XX 15-NOV-1994; 94JP-0280655.
 PR
 XX
 XX (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
 PA
 XX
 XX WPI; 1996-316314/32.
 DR
 XX P-PSDB; AAR99141.
 XX
 XX DNA encoding ligand-binding region contg. the CRH region of
 PT granulocyte-colony stimulating factor receptor - useful in
 PT treatment of leukaemia resulting from proliferation of granulocytes

XX
 PS
 XX Claim 4; Page 12-14; 17pp; Japanese.
 CC
 CC AAT35138 encodes a human protein of a ligand binding region of a G-CSF
 CC (granulocyte colony stimulating factor) receptor. The DNA and protein
 CC are used in the development and/or study of drugs which can be
 CC substituted for G-CSF. Such drugs are useful in the treatment of
 CC leukaemia resulting from granulocyte over-proliferation. The DNA may
 CC be expressed recombinantly to provide a high yield of the protein.
 XX
 XX Sequence 999 BP; 207 A; 347 C; 276 G; 169 T; 0 other;
 SQ

Query Match 92.0%; Score 13.8; DB 17; Length 999;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
 :||||:|||||
 Db 966 GCTCCAGTCGCTCCA 952

RESULT 8
 AAQ67887/c
 ID AAQ67887 standard; DNA; 1193 BP.
 XX
 XX AAQ67887;
 AC
 XX
 XX 27-MAR-1995 (first entry)
 DT
 XX
 XX Rat ciliary neutrophic factor-alpha DNA.
 DE
 XX
 XX Ciliary neutrophic factor; neurological disease; haemorrhage; tumor;
 KW trauma; infection; Alzheimer's disease; Creutzfeld Jakob disease;
 KW Down's syndrome; central nervous system; ds.
 XX
 XX Rattus rattus.
 OS
 XX
 XX Key Location/Qualifiers
 FH 81.1058
 FT /*tag- a
 FT
 XX W09416721-A.
 PN
 XX
 XX 04-AUG-1994.
 PD
 XX
 XX 28-JAN-1994; 94WO-US01057.
 PF
 XX
 XX 29-JAN-1993; 93US-0010978.
 PR
 XX
 XX (REGE-) REGENERON PHARM INC.
 PA
 XX
 XX Friedman B, Ip NV, Rudge J, Wiegand S, Yancopoulos GD;
 PI
 XX WPI; 1994-263772/32.
 DR
 XX P-PSDB; AAR58304.
 DR
 XX
 XX Promoting survival and proliferation of neurons to - with
 PT recombinant human ciliary neurotrophic factor, also new rat
 PT receptor for this factor, useful to treat neurological disorders
 PT
 XX
 XX Claim 5; Fig.1; 49pp; English.
 PS
 XX
 XX Survival and/or proliferation of corticospinal neurons or neurons in
 CC the subependymal zone in a patient are promoted by administration of
 CC recombinant ciliary neurotrophic factor. The protein may be
 CC used to treat a wide range of neurological diseases, e.g haemorrhage,
 CC tumor, trauma, infection, Alzheimer's disease, Creutzfeld Jakob
 CC disease, Down's syndrome, etc.
 XX
 XX Sequence 1193 BP; 267 A; 382 C; 304 G; 240 T; 0 other;
 SQ

```

RESULT 4
AAZ43552
ID AAZ43552 standard; DNA; 22 BP.
XX
AC AAZ43552;
XX
DT 21-FEB-2000 (first entry)
XX
DE Human OB-R PCR primer 2.
XX
KW OB-R; leptin; PCR primer; differentiation; bone marrow; osteopathic;
KW stromal progenitor; osteoblastic lineage; treatment; osteoporosis; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN WO9953939-A1.
XX
PD 28-OCT-1999.
XX
PF 20-APR-1999; 99WO-US08604.
XX
PR 20-APR-1998; 98US-0082320.
XX
PA (MAYO-) MAYO FOUNDATION.
XX
PI Burguera B, Thomas T, Riggs BL;
XX
DR WPI; 2000-052683/04.
XX
PT Inducing differentiation of bone marrow stromal progenitor cells to an
PT osteoblastic lineage
XX
PS Example 2; Page 17; 47pp; English.
XX
CC This invention describes a novel method (A) of inducing differentiation
CC of a bone marrow stromal progenitor cell to an osteoblastic lineage is
CC new and comprises contacting the bone marrow stromal progenitor cell with
CC an amount of leptin or its analog. The products of the invention have
CC osteopathic activity. The method is useful for inducing differentiation
CC of a bone marrow stromal progenitor cell to an osteoblastic lineage and
CC for inducing bone formation in mammals. Therefore the method is useful
CC for the treatment of osteoporosis and other conditions where bone
CC formation is required. This sequence represents a PCR primer used in the
CC amplification of human OB-R variants.
XX
SQ Sequence 22 BP; 5 A; 9 C; 2 G; 6 T; 0 other;

Query Match 92.0%; Score 13.8; DB 21; Length 22;
Best Local Similarity 80.0%; Pred. NO. 1.4e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
:||||:|||||
Db 2 actccagtcactcca 16

RESULT 5
AAT33516/C
ID AAT33516 standard; cDNA to mRNA; 639 BP.
XX
AC AAT33516;
XX
DT 24-OCT-1996 (first entry)
XX
DE Human G-CSF receptor ligand binding region C-terminus coding sequence.
XX
KW Granulocyte colony stimulating factor; G-CSF; C-terminus; mouse; human;
KW ligand binding domain; E.coli; maltose binding protein; receptor;
KW G-CSF-dependent disease; G-CSF abnormality; ss.
XX

```

```

OS Homo sapiens.
XX
PN JP08131172-A.
XX
PD 28-MAY-1996.
XX
PF 14-NOV-1994; 94JP-0278841.
XX
PR 14-NOV-1994; 94JP-0278841.
XX
PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
XX
DR WPI; 1996-303849/31.
XX
DR P-PSDB; AAW00648.
XX
PT DNA coding for a ligand-binding region BC of G-CSF receptor
PT useful for prevention or treatment of G-CSF diseases
XX
PS Claim 2; Page 9-10; 11pp; Japanese.
XX
CC This sequence represents the C-terminal domain of a ligand binding
CC region of a human granulocyte colony stimulating factor (G-CSF) receptor.
CC This sequence, the corresponding mouse sequence (see AAT33515), or a
CC conserved fragment of both these sequences (see AAT33517) can be used in
CC an expression vector for the production of the receptor. The sequences
CC can also be used in an expression vector containing E.coli maltose
CC binding protein to produce a fusion protein. The DNA can be used in the
CC study of diseases related to the interaction between the G-CSF receptor
CC and its ligand, as well as for the treatment or prevention of
CC G-CSF-dependent diseases and abnormalities. The recombinant
CC ligand-binding region produced, is physiologically active and can be used
CC in the study of the G-CSF receptor, such as analysis of its
CC stereostructure.
XX
SQ Sequence 639 BP; 135 A; 227 C; 174 G; 103 T; 0 other;

Query Match 92.0%; Score 13.8; DB 17; Length 639;
Best Local Similarity 80.0%; Pred. NO. 1.8e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
:||||:|||||
Db 606 GCTCCAGTCGCTCCA 592

RESULT 6
AAT68830/C
ID AAT68830 standard; cDNA to mRNA; 990 BP.
XX
AC AAT68830;
XX
DT 04-FEB-1998 (first entry)
XX
DE cDNA for rheumatoid arthritis auto-antigen clone A.
XX
KW Rheumatoid arthritis; auto-antigen; clone A; diagnosis;
KW prediction; synovial cell; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..990
FT /tag= a
XX
PN WO9717441-A1.
XX
PD 15-MAY-1997.
XX
PF 06-NOV-1996; 96WO-JP03250.
XX
PR 07-NOV-1995; 95JP-0288957.
XX

```

PS Claim 12; Page 51; 87pp; English.

XX 5 Degenerate hybridisation probes (AA17870-74) are based on a
 CC conserved motif (AAR92812) found in haemopoietin receptors. The
 CC probes are used in the identification and/or cloning of genes
 CC coding for novel haemopoietin receptors, e.g. the murine
 CC interleukin-11 (IL-11) receptor alpha chain gene (AA17868). Such
 CC receptors are defined by their ability to hybridise to the
 CC probes under medium stringency conditions.

XX Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;

Query Match 92.0%; Score 13.8; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
 DB 1 rctccartcrctcca 15

RESULT 2
 AAT64433
 ID AAT64433 standard; DNA; 15 BP.
 AC AAT64433;
 XX
 DT 30-OCT-1997 (first entry)
 DE
 XX Haemopoietin receptor NR2 hybridising oligonucleotide HYB2.
 KW Haemopoietin receptor; new receptor 2; NR2; leptin; human;
 KW autoimmune disease; nervous system; cerebral palsy;
 KW trauma induced paralysis; vascular ischaemia; stroke;
 KW neuronal tumour; motor neurone disease; Parkinson's disease;
 KW Huntington's disease; Alzheimer's disease; multiple sclerosis;
 KW peripheral neuropathy; heavy metal; alcohol; toxicity;
 KW kidney failure; infectious disease; herpes; rubella; measles;
 KW chicken pox; HIV; HTLV-1; therapy; probe; ss.
 XX
 OS Synthetic.
 XX
 PN WO9712037-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 26-SEP-1996; 96WO-AU00607.
 XX
 PR 26-SEP-1995; 95AU-0005641.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PI Alexander WS, Gainsford T, Hilton DJ, Metcalf D;
 PI Ng A, Nicola NA, Willson T;
 XX
 DR WPI; 1997-212896/19.
 XX
 PT Human haemopoietin receptor NR2, and corresponding DNA - used e.g.
 PT for treatment of autoimmune diseases
 XX
 PS Claim 1; Page 68; 96pp; English.

XX Oligonucleotide HYB2 hybridises under medium stringent conditions
 CC to a novel DNA (see AAT64442) encoding human haemopoietin receptor
 CC NR2 (AAW14841). It was used in the isolation of a partial NR2
 CC sequence from a cDNA library constructed from the bone marrow
 CC mRNA of a patient recovering from chemotherapy. NR2 and genetic
 CC sequences encoding it can be used in the development of
 CC (ant)agonists, therapeutics and diagnostic reagents based on
 CC ligand interaction with the receptor.

XX Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;

Query Match 92.0%; Score 13.8; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
 DB 1 rctccartcrctcca 15

RESULT 3
 AAV27138
 ID AAV27138 standard; DNA; 15 BP.
 XX
 AC AAV27138;
 XX
 DT 29-SEP-1998 (first entry)
 DE
 XX Novel haemopoietin receptor probe 1.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
 KW probe.
 XX
 OS Synthetic.
 OS Mammalian.
 XX
 PN WO9811225-A2.
 XX
 PD 19-MAR-1998.
 XX
 PF 11-SEP-1997; 97WO-GB02479.
 XX
 PR 11-SEP-1996; 96AU-0002246.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIEGLEWSKA H E.
 XX
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y;
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T;
 PI Zhang J;
 XX
 DR WPI; 1998-260970/23.
 XX
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 XX
 PS Claim 3; Page 132; 182pp; English.

XX The probes AAV27138 and AAV27139 are used to identify nucleic acid
 CC molecules encoding a novel haemopoietin receptor (HR). Interaction
 CC between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.

XX Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;

Query Match 92.0%; Score 13.8; DB 19; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
 DB 1 rctccartcrctcca 15

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 20:16:40 ; Search time 301.32 Seconds
(without alignments)
31.258 Million cell updates/sec

Title: US-09-532-263-7

Perfect score: 15

Sequence: 1 RCTCCARTCRCTCCA 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.*
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22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.8	92.0	15	AAT17871	Haemopoietin recep
2	13.8	92.0	15	AAT64433	Haemopoietin recep
3	13.8	92.0	15	AAV27138	Novel haemopoietin
4	13.8	92.0	22	AAZ43552	Human OB-R PCR pri
5	13.8	92.0	639	AAZ43552	Human G-CSF recept
6	13.8	92.0	990	AAT68830	cDNA for rheumatoid
7	13.8	92.0	999	AAT35138	DNA encoding cytok
8	13.8	92.0	1193	AAQ67887	Rat ciliary neutro
9	13.8	92.0	1383	AAQ66164	Mouse interleukin-
10	13.8	92.0	1419	AAZ76452	Human ORFX ORF2007
11	13.8	92.0	1591	AAQ20195	Ciliary neurotroph

c 12	13.8	92.0	1591	14	AAQ39626	Sequence encoding
c 13	13.8	92.0	1591	16	AAQ83223	Human recombinant
c 14	13.8	92.0	1977	17	AAT14602	Human gp130 splice
c 15	13.8	92.0	2096	19	AAV69318	M. fortuitum plasm
c 16	13.8	92.0	2119	22	AAQ92350	Human haemopoietin
c 17	13.8	92.0	2369	17	AAQ74081	gp130 N-terminal f
c 18	13.8	92.0	2440	22	AAQ92338	Human haemopoietin
c 19	13.8	92.0	2461	18	AAT75707	Murine leptin rece
c 20	13.8	92.0	2497	15	AAQ55941	Murine leukaemia i
c 21	13.8	92.0	2498	13	AAQ25800	MLIF-R. Mus muscu
c 22	13.8	92.0	2498	15	AAQ58426	Mouse LIF-R clone
c 23	13.8	92.0	2498	16	AAQ92271	Murine leukaemia i
c 24	13.8	92.0	2507	18	AAT98534	Natural splice var
c 25	13.8	92.0	2529	12	AAQ13857	Human G-CSF recept
c 26	13.8	92.0	2529	18	AAT75703	Murine leptin rece
c 27	13.8	92.0	2546	12	AAQ11579	Encodes granulocyt
c 28	13.8	92.0	2546	18	AAQ74099	Human granulocyte
c 29	13.8	92.0	2562	16	AAQ95481	G-CSFR cDNA clone
c 30	13.8	92.0	2624	18	AAT98532	Coding sequence fo
c 31	13.8	92.0	2685	18	AAT97149	Ob protein recepto
c 32	13.8	92.0	2685	18	AAT97156	Ob protein recepto
c 33	13.8	92.0	2703	18	AAT75706	Murine leptin rece
c 34	13.8	92.0	2754	17	AAT14603	Human gp130 native
c 35	13.8	92.0	2868	18	AAT85578	Murine WSX recepto
c 36	13.8	92.0	2877	17	AAT12913	Haematopoietin rec
c 37	13.8	92.0	2877	18	AAT95781	Human OB-R variant
c 38	13.8	92.0	2880	17	AAT12912	Haematopoietin rec
c 39	13.8	92.0	2880	18	AAT95780	Human OB-R variant
c 40	13.8	92.0	2880	18	AAT74022	Variant form of hu
c 41	13.8	92.0	2931	12	AAQ11580	Clone 25-1 encodes
c 42	13.8	92.0	2933	18	AAT47100	Human granulocyte
c 43	13.8	92.0	2942	12	AAQ13856	Human G-CSF recepto
c 44	13.8	92.0	2943	21	AAQ62841	Human granulocyte
c 45	13.8	92.0	2948	18	AAT98533	Coding sequence fo

ALIGNMENTS

RESULT 1

AAT17871
ID AAT17871 standard; DNA; 15 BP.

XX AAT17871;

XX 21-MAY-1996 (first entry)

DE Haemopoietin receptor probe HYB2.

XX Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
therapy; diagnosis; probe; hybridisation; ss.

OS Synthetic.

XX WO9607737-A1.

PD 14-MAR-1996.

XX 05-SEP-1995; 95WO-AU00578.

PR 05-SEP-1994; 94AU-0007902.

PR 05-SEP-1994; 94AU-0007901.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Hilton DJ;

XX WPI; 1996-171612/17.

PT Nucleic acid encoding haemopoietin receptor containing conserved
amino acid motif esp. IL-11 receptor alpha chain - used for
developing IL-11 (ant)agonists

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/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
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Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
Db 161 GCTCCAGTCGCTCCA 175

RESULT 15
FR0028454/c
LOCUS      FR0028454      360 bp      DNA      GSS      25-JUN-1998
DEFINITION Fugu rubripes GSS sequence, clone 006118BD2, genomic survey
sequence.
ACCESSION  AL024826
VERSION    AL024826.1 GI:3262169
KEYWORDS  GSS: genome survey sequence.
SOURCE    Takifugu rubripes.
ORGANISM  Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 360)
Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrانيا, Y.,
Williams, G. and Brenner, S.
Direct Submission
Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridge, CB10 1SB, UK. Email:
biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
FEATURES
source      Location/Qualifiers
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/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 006118"
/clone="006118BD2"
BASE COUNT      87 a      85 c      91 g      92 t      5 others
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Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
Db 169 GCTCCAGTCGCTCCA 155

Search completed: August 29, 2001, 19:22:13
Job time: 24136 sec
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ORGANISM      Caenorhabditis briggsae
               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
REFERENCE      1 (bases 1 to 352)
AUTHORS        Hillier,L., Chiapelli,B., Chissee,S., Clark,N., Couch,J., Dubuque
               T., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Kuwabara,P., Le
               M., Mardis,E., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan
               F., Treviskis,E., Waterston,R., Wohlmann,P. and Wilson,R.
TITLE          Washington University Caenorhabditis briggsae EST project
JOURNAL        Unpublished (1995)
COMMENT        Contact: Marra MA
               Washington University Genome Sequencing Center
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1455
               Fax: 314 286 1810
               Email: mmarra@watson.wustl.edu
               PCR_F: TGTAAACGACGCCAGTCAGCAAGTTCCAGCGCTG
               PCR_B: CAGGAACAGCTATGACCTATGACTATTTCTCCAGGTA
               Source: Washington University Genome Sequencing Center
               PCR amplified DNA is available from Washington University Genome
               Sequencing Center. Aliquots of the library may be requested from P.
               Kuwabara (pekemrc-lmb.cam.ac.uk).
               Seq primer: Commercially available M13 reverse dye primer.
FEATURES       Location/Qualifiers
               1..352
               /organism="Caenorhabditis briggsae"
               /strain="G16 Gujarat"
               /db_xref="taxon:6238"
               /clone_lib="Kuwabara Mixed stage C. briggsae"
               /note="Vector: Lambda gt10; Site_1: EcoRI; Site_2: EcoRI;
               Stage:mixed, Sex:hermaphrodite. Library construction:
               First strand oligo(dT) primed. Second strand was as per
               Gubler/Hoffman. Ligated to EcoRI adaptors. Library is
               non-directed. Library is non-normalized. Library
               constructed by P.E. Kuwabara. Additional details on
               construction of the library are described in P.E.
               Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor
               sequence: GAATTC CGTTCGTCG"
BASE COUNT     94 a 52 c 119 g 84 t 3 others
ORIGIN

Query Match      92.0%; Score 13.8; DB 187; Length 352;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
      :||||:|||||
Db 317 ACTCCAATCACTCCA 303

RESULT 13
AA272591/c
LOCUS      AA272591 355 bp mRNA EST 26-MAR-1997
DEFINITION va75c12_r1 Soares mouse NML Mus musculus cDNA clone IMAGE:737206 5'
            similar to gb:D17444 Mouse mRNA for soluble D-factor/LIF receptor,
            complete (MOUSE);, mRNA sequence.
ACCESSION  AA272591
VERSION     AA272591.1 GI:1910922
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 355)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R..
TITLE       The WashU-HHMI Mouse EST Project
JOURNAL     Unpublished (1996)

Caenorhabditis briggsae
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
1 (bases 1 to 352)
AUTHORS Hillier,L., Chiapelli,B., Chissee,S., Clark,N., Couch,J., Dubuque
T., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Kuwabara,P., Le
M., Mardis,E., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan
F., Treviskis,E., Waterston,R., Wohlmann,P. and Wilson,R.
TITLE Washington University Caenorhabditis briggsae EST project
JOURNAL Unpublished (1995)
COMMENT Contact: Marra MA
Washington University Genome Sequencing Center
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1455
Fax: 314 286 1810
Email: mmarra@watson.wustl.edu
PCR_F: TGTAAACGACGCCAGTCAGCAAGTTCCAGCGCTG
PCR_B: CAGGAACAGCTATGACCTATGACTATTTCTCCAGGTA
Source: Washington University Genome Sequencing Center
PCR amplified DNA is available from Washington University Genome
Sequencing Center. Aliquots of the library may be requested from P.
Kuwabara (pekemrc-lmb.cam.ac.uk).
Seq primer: Commercially available M13 reverse dye primer.
FEATURES Location/Qualifiers
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/note="Vector: Lambda gt10; Site_1: EcoRI; Site_2: EcoRI;
Stage:mixed, Sex:hermaphrodite. Library construction:
First strand oligo(dT) primed. Second strand was as per
Gubler/Hoffman. Ligated to EcoRI adaptors. Library is
non-directed. Library is non-normalized. Library
constructed by P.E. Kuwabara. Additional details on
construction of the library are described in P.E.
Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor
sequence: GAATTC CGTTCGTCG"
BASE COUNT 94 a 52 c 119 g 84 t 3 others
ORIGIN

Query Match      92.0%; Score 13.8; DB 4; Length 355;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
      :||||:|||||
Db 104 GCTCCAGTCACCTCCA 90

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LOCUS      C65854 360 bp mRNA EST 22-SEP-1997
DEFINITION C65854 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
            clone yk395h5 5', mRNA sequence.
ACCESSION  C65854
VERSION     C65854.1 GI:2424559
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans.
            Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            Rhabditidae; Peloderinae; Caenorhabditis.
            Kohara,Y., Motobashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
            M., Miyata,A. and Nishigaki,A.
            Expression map of the C.elegans genome
            Unpublished (1996)
            Contact: Yuji Kohara
            Gene Library Lab
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
FEATURES       Location/Qualifiers
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               /organism="Caenorhabditis elegans"
               /strain="Cbl489 him-8(e1489)"
               /db_xref="taxon:6239"
               /clone="yk395h5"
               /clone_lib="Yuji Kohara unpublished cDNA"

```

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:454254
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 209.

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/tissue_type="Liver"
/lab_host="DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified
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was primed with a Not I - oligo(dT) primer 15'
TGTACCAATCTGAAGTGGAGCGCGCGAATCTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

BASE COUNT 96 a 89 c 76 g 94 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 4; Length 355;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
:||||:|||||
Db 104 GCTCCAGTCACCTCCA 90

RESULT 14
C65854
LOCUS C65854 360 bp mRNA EST 22-SEP-1997
DEFINITION C65854 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
clone yk395h5 5', mRNA sequence.
ACCESSION C65854
VERSION C65854.1 GI:2424559
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
Rhabditidae; Peloderinae; Caenorhabditis.
Kohara,Y., Motobashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES source
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Location/Qualifiers
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/clone_lib="Yuji Kohara unpublished cDNA"

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

```

project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-mr1-CT0355-180
200-006-cl2st3=2000-02-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 242.
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1..242
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/clone_lib="CT0355"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      65 a      58 c      40 g      79 t
ORIGIN
Query Match      92.0%; Score 13.8; DB 121; Length 242;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY      1  RCTCCATRCRCTCCA 15
          :||||:|||||
Db      163  ACTCCAGTCACTCCA 177

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AI907996	254 bp	mRNA	EST	30-MAR-2000
IL-BT161-080399-010	BT161	Homo sapiens	CDNA	mrna sequence.
AI907996				
AI907996.1	GI:6498676			
EST.				
human.				
Homo sapiens				
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1 (bases 1 to 254)				
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.				
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
20202663				
Contact: Simpson A.J.G.				
Laboratory of Cancer Genetics				
Ludwig Institute for Cancer Research				
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil				
Tel: +55-11-2704922				

Email: genome-resetrc.riken.go.jp,
 URL:http://genome.rtc.riken.go.jp/
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
 N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermostabilization and thermoactivation of thermostable enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Kitsumi,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
 Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.

FEATURES

source
 Location/Qualifiers
 1. .181
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="A330054L14"
 /clone_lib="RIKEN full-length enriched, adult male spinal
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 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Site.1: SalI; Site.2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGAGCTTTTTTTTTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 459.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGATTCGAGTTAATTAATCCCCCCCCCCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pBluescript KS(+) after bulk excision from Lambda
 FIC I."

BASE COUNT 50 a 56 c 29 g 46 t
 ORIGIN

Query Match 92.0%; Score 13.8; DB 127; Length 181;
 Best Local Similarity 80.0%; Pred. No. 2.3e+03;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCTCCARTCRCTCCA 15
 :|||||:|||||
 Db 51 ACTCCAGTCACTCCA 65

RESULT 3
 AT002416 199 bp mRNA EST 10-SEP-1999
 LOCUS AT002416 Entamoeba histolytica trophozoite Entamoeba histolytica
 DEFINITION cDNA clone En044, mRNA sequence.
 ACCESSION AF002416
 VERSION AF002416.1 GI:5865820
 KEYWORDS EST.
 SOURCE Entamoeba histolytica.
 ORGANISM Entamoeba histolytica.
 Eukaryota; Entamoebidae; Entamoeba.
 REFERENCE 1 (bases 1 to 199)
 AUTHORS Kim,T.O., Hong,Y.C., Yu,H.S., Hwang,M.Y., Yun,H.C., Kong,H.H. and
 Chung,D.I.
 TITLE Entamoeba histolytica trophozoite EST

JOURNAL COMMENT

Unpublished (1999)
 Contact: Chung DI
 Department of Parasitology
 Kyungpook National University School of Medicine
 Dong-in dong 101, Chung-gu, Taegu 700 - 422, Republic of Korea
 Tel: 82-53-420-6958
 Fax: 82-53-422-9330
 Email: dichungdbh.kyungpook.ac.kr
 Submitted through BRIC(Biological Research Information Center) of
 Korea
 URL: <http://bric.postech.ac.kr/>.

FEATURES

source
 Location/Qualifiers
 1. .199
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 /dev_stage="trophozoite"
 /lab_host="XLI blue"
 /note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 82 a 33 c 38 g 45 t 1 others
 ORIGIN

Query Match 92.0%; Score 13.8; DB 106; Length 199;
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCARTCRCTCCA 15
 :|||||:|||||
 Db 12 GCTCCAGTCACTCCA 26

RESULT

BB018457 232 bp mRNA EST 22-JUN-2000
 LOCUS BB018457 RIKEN full-length enriched, adult male testis (DH10B) Mus
 DEFINITION musculus cDNA clone 4930578B11 3', mRNA sequence.
 BB018457
 ACCESSION BB018457.1 GI:8190064
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
 1 (bases 1 to 232)
 Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
 P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
 Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
 Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
 Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
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 Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
 Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
 Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya
 T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yananaka,I.,
 Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
 M., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Konno,H., et al.)
 Unpublished (2000)

TITLE

JOURNAL
 COMMENT
 Contact: Yoshihide Hayashizaki
 Genome Exploration Research Group, Life Science Tsukuba Center,
 Genome Science Laboratory
 The Institute of Physical and Chemical Research (RIKEN), Genomic
 Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: +81-298-36-9013
 Fax: +81-298-36-9098
 Email: genome-resetrc.riken.go.jp,
 URL:<http://genome.rtc.riken.go.jp/>
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	13.8	92.0	140	115	AW408083	AW408083 UT-HF-BMO
2	13.8	92.0	181	127	BB189498	BB189498 BB189498
3	13.8	92.0	199	106	AT002416	AT002416 AT002416
4	13.8	92.0	232	123	BB018457	BB018457 BB018457
5	13.8	92.0	242	121	AA859572	AA859572 MRI-CT035
6	13.8	92.0	254	103	AI907996	AI907996 IL-BF161-
7	13.8	92.0	279	129	BB258685	BB258685 BB258685
8	13.8	92.0	281	121	AA859532	AA859532 MRI-CT035
9	13.8	92.0	295	161	BB59621	BB59621 BB59621
10	13.8	92.0	321	163	BE080913	BE080913 QV1-BT063
11	13.8	92.0	331	128	BB209387	BB209387 BB209387
12	13.8	92.0	352	187	R04486	R04486 pk24c12.r1
13	13.8	92.0	355	4	AA272591	AA272591 va75c12.r
14	13.8	92.0	360	156	C65854	C65854 C65854 Yuj1
15	13.8	92.0	360	222	FR0028454	FR0028454 Fugu rubr
16	13.8	92.0	364	30	AV401050	AV401050 AV401050
17	13.8	92.0	368	32	AV698306	AV698306 AV698306
18	13.8	92.0	381	14	AA984710	AA984710 am90a11.s
19	13.8	92.0	387	116	AA489097	AA489097 UT-M-BH3-
20	13.8	92.0	398	169	BF760838	BF760838 RC4-CT010
21	13.8	92.0	408	169	AA663262	AA663262 ab80f07.s
22	13.8	92.0	408	223	AQ060441	AQ060441 CIT-HSP-2
23	13.8	92.0	417	31	AV523125	AV523125 AV523125
24	13.8	92.0	423	110	AV743168	AV743168 AV743168
25	13.8	92.0	424	159	N75185	N75185 Yw33a04.r1
26	13.8	92.0	424	168	BF706981	BF706981 281663 MA
27	13.8	92.0	426	175	BG263754	BG263754 WHE2348.F
28	13.8	92.0	428	231	AQ663435	AQ663435 HS-2160_B
29	13.8	92.0	435	227	AQ332979	AQ332979 HS-5005_B
30	13.8	92.0	435	231	AQ667104	AQ667104 HS-2106_B
31	13.8	92.0	444	9	AA619632	AA619632 v154d09.r
32	13.8	92.0	446	2	AA082811	AA082811 zn25a04.r
33	13.8	92.0	448	8	AA495324	AA495324 fa01c03.r
34	13.8	92.0	453	188	R73050	R73050 yj94f12.r1
35	13.8	92.0	455	114	AW279627	AW279627 fj42c06.x
36	13.8	92.0	455	188	T21895	T21895 3903 Lambda
37	13.8	92.0	456	239	AZ151949	AZ151949 SP-0006.B
38	13.8	92.0	458	170	BF820788	BF820788 MRI-RT004
39	13.8	92.0	459	223	AQ022781	AQ022781 HS-2180_A
40	13.8	92.0	462	231	AQ648347	AQ648347 RPI193-EC
41	13.8	92.0	463	18	A1311382	A1311382 q088e12.x
42	13.8	92.0	467	169	BF776672	BF776672 287536 MA
43	13.8	92.0	471	106	AT005091	AT005091 AT005091
44	13.8	92.0	477	145	BF200134	BF200134 WHE2252.D
45	13.8	92.0	482	231	AQ668275	AQ668275 HS-2121_B

ALIGNMENTS

RESULT	1
LOCUS	AW408083
DEFINITION	UI-HF-BMO-adu-d-10-0-UT.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062850 5', mRNA sequence.
ACCESSION	AW408083
VERSION	AW408083.1 GI:6927140
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 140)
TITLE	NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

Location/Qualifiers

1. 140

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3062850"

/clone_lib="NIH_MGC_38"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTI)"

/note="vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (2.5-3.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

30 a 57 c 29 g 24 t

BASE COUNT
ORIGIN

Query Match 92.0%; Score 13.8; DB 115; Length 140;

Best Local Similarity 80.0%; Pred. No. 2.3e+03;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTCCARTCRCTCCA 15
:|||||:|||||

Db 102 ACTCCAGTCACTCCA 116

RESULT 2

BB189498

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Yoshihide Hayashizaki

Genome Exploration Research Group, Life Science Tsukuba Center,

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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: +81-298-36-9013

Fax: +81-298-36-9098

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:22:10 ; Search time 3770.35 seconds
(without alignments)
37.607 Million cell updates/sec

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Perfect score: 15
Sequence: 1 RCTCCARTCRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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17. .697
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KRSPLETRALTEVESELEQLFLIFREDLMLKMDSLQDIKALITGLFVQDNV
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HLGDGVAMAHADALDDFDLMDGDSFGPGFTPHDSAPYGALDMADFEFEQMFTDA
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BASE COUNT 147 a 241 c 194 g 119 t
ORIGIN
Query Match      88.0%; Score 13.2; DB 9; Length 701;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGCRCTCCA 15
:||||| ||:|||||
Db 212 GCTCCAGGCGCTCCA 198

RESULT 14
LOCUS      MMU272227/c      701 bp      mRNA      17-FEB-2000
DEFINITION Mus musculus mRNA for beta-A2-crystallin (cryba2 gene).
ACCESSION  AJ272227
VERSION     AJ272227.1 GI:7007338
KEYWORDS   beta-A2-crystallin; CRYBA2 gene.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 701)
AUTHORS   Gray,J.
TITLE     Sequence analysis of bata-A2-, beta-A4- and beta-B3-crystallin cDNA
          completes the identification of the members of this gene family in
          the mouse
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 701)
AUTHORS   Gray,J.
TITLE     Direct Submission
JOURNAL   Submitted (16-FEB-2000) Gray J., Institute of Mammalian Genetics,
          GSF-National Research Center for Environment and Health,
          Ingolstaedter Landstr. 1, D-86764 Neuherberg, GERMANY

FEATURES             location/Qualifiers
source               1. .701
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BASE COUNT 151 a 206 c 206 g 138 t
ORIGIN

Query Match      88.0%; Score 13.2; DB 94; Length 701;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 RCTCCANGCRCTCCA 15
:||||| ||:|||||
Db 309 GCTCCAGGCGCTCCA 295

RESULT 15
LOCUS      AF081273/c      704 bp      mRNA      MAM      03-MAR-1999
DEFINITION Bos taurus interleukin-4 receptor alpha chain mRNA, partial cds.
ACCESSION  AF081273
VERSION     AF081273.1 GI:4322316
KEYWORDS   cow.
SOURCE     Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
            Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 704)
AUTHORS   Trigona,W.T. and Estes,D.M.
TITLE     Cloning of bovine homolog to interleukin-4 receptor alpha chain
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 704)
AUTHORS   Trigona,W.T. and Estes,D.M.
TITLE     Direct Submission
JOURNAL   Submitted (29-JUL-1998) Veterinary Pathobiology, University of
            Missouri-Columbia, 201 Conaway Hall, Columbia, MO 65211, USA

FEATURES             location/Qualifiers
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                    HADISHTWLLTWNPNYPSNLYSELTVLNINSENDPTDFTYNTYMGPTLRVAAS
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BASE COUNT 171 a 223 c 184 g 126 t
ORIGIN

Query Match      88.0%; Score 13.2; DB 7; Length 704;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGCRCTCCA 15
:||||| ||:|||||
Db 561 GCTCCAGGCGCTCCA 547

Search completed: August 29, 2001, 19:52:00
Job time: 17238 sec
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entry [NCBI gibbsq 168377] from the original journal article.
This sequence comes from Fig. 5.

FEATURES

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CDS

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BASE COUNT 192 a 164 c 154 g 159 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 97; Length 669;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15

Db 585 ACTCCATGCACCTCCA 571

RESULT 11

BOVBA2/c
LOCUS BOVBA2 696 bp mRNA MAM 26-APR-1993
DEFINITION Cow beta-A2 crystallin (beta-A2) mRNA, complete cds.
ACCESSION M60329
VERSION M60329.1 GI:162726
KEYWORDS beta-A2-crystallin; crystallin.
SOURCE Bos taurus CDNA to mRNA.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 696)
AUTHORS van Rens, G.L.M., Driessen, H.P.C., Nalini, V., Slingsby, C., de Jong, W.W. and Bloemendal, H.
TITLE Isolation and characterization of cDNAs encoding beta-A2- and beta-A4-crystallins: Heterologous interactions in the predicted beta-A4-beta-B2 heterodimer
JOURNAL Gene 102, 179-188 (1991)
MEDLINE 91340151
FEATURES Location/Qualifiers
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BASE COUNT 131 a 226 c 212 g 127 t
ORIGIN

polyA_signal

BASE COUNT

131 a 226 c 212 g 127 t

ORIGIN

Query Match

Best Local Similarity 88.0%; Score 13.2; DB 7; Length 696;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15

Db 291 GCTCCAGGCACTCCA 277

RESULT 12

AF166331/c
LOCUS AF166331 700 bp mRNA PRI 22-JUL-1999
DEFINITION Homo sapiens beta crystallin A2 (CRYBA2) mRNA, complete cds.
ACCESSION AF166331
VERSION AF166331.1 GI:5566395
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 700)
AUTHORS Wistow, G.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1999) Molecular Structure and Function, National Eye Institute, 6/331, National Institutes of Health, Bethesda, MD 20892-2740, USA
FEATURES Location/Qualifiers
source
1..700
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..700
/gene="CRYBA2"
30..623
/gene="CRYBA2"
/note="lens structural protein"
/codon_start=1
/product="beta crystallin A2"
/protein_id="AAD45388.1"
/db_xref="GI:5566396"
/translation="MSSAPAGPAPASLTLMDEDFQGRRCRLSDCANIGERGGLPR
VRSKVGWVAFEYDFQGGQFLEKGDYPRWSAWSGAGHSDDLSPRVLCAN
HNSDRVTLFEGNFGQCKFLNDDYPSLPSMGWASKDVGSLKSSGAWVAYQYPGYRG
YQYVLERDHSGEFCTYGEQTGQHTGQLSIRRVQH"
BASE COUNT 145 a 223 c 212 g 120 t
ORIGIN

Query Match

Best Local Similarity 88.0%; Score 13.2; DB 89; Length 700;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15

Db 275 ACTCCAGGCACTCCA 261

RESULT 13

A64741/c
LOCUS A64741 701 bp DNA PAT 29-MAR-1999
DEFINITION Sequence 1 from Patent WO9730164.
ACCESSION A64741
VERSION A64741.1 GI:4530777
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 701)
AUTHORS Haseloff, J. P. and Hodge, S.
TITLE IMPROVEMENTS IN OR RELATING TO GENE EXPRESSION
JOURNAL Patent: WO 9730164-A 1 21-AUG-1997;
MEDICAL RES COUNCIL (GB)
COMMENT Other publication AU 1801497 19970902.
FEATURES Location/Qualifiers

REFERENCE 78026 Versailles, France
 AUTHORS 2 (bases 1 to 600)
 TITLE Genoscope.
 JOURNAL Direct Submission
 Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
 CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)

COMMENT The cDNA library to be analyzed within the framework of this
 project was created using a Botrytis cinerea strain which was grown
 under conditions of nitrogen deprivation, which is the normal
 situation for B. cinerea during its development on its host plant.
 The library was produced in an oriented direction, in the pBSII
 vector.

FEATURES

source

Location/Qualifiers
 1. .600
 /organism="Botryotinia fuckeliana"
 /strain="T4"
 /db.xref="taxon:40559"
 /note="Genoscope sequence ID : W06A041"
 BASE COUNT 169 a 131 c 142 g 158 t
 ORIGIN

Query Match 88.0%; Score 13.2; DB 14; Length 600;
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGCRCTCCA 15
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 Db 16 ACTCCAAGCACTCCA 30

RESULT 8

CNS01ACZ 600 bp mRNA PLN 02-SEP-1999
 LOCUS Botrytis cinerea strain T4 cDNA library under conditions of
 nitrogen deprivation.

ACCESSION AL112779.1 GI:5827398
 VERSION cDNA library; nitrogen deprivation.
 KEYWORDS Botryotinia fuckeliana.
 SOURCE Botryotinia fuckeliana.

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
 Helotiales; Sclerotiniaceae; Botryotinia.

REFERENCE 1 (bases 1 to 600)
 AUTHORS Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
 TITLE Direct Submission
 JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
 78026 Versailles, France

REFERENCE 2 (bases 1 to 600)

Genoscope.
 Direct Submission
 Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
 CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)

COMMENT The cDNA library to be analyzed within the framework of this
 project was created using a Botrytis cinerea strain which was grown
 under conditions of nitrogen deprivation, which is the normal
 situation for B. cinerea during its development on its host plant.
 The library was produced in an oriented direction, in the pBSII
 vector.

FEATURES

source

Location/Qualifiers
 1. .600
 /organism="Botryotinia fuckeliana"
 /strain="T4"
 /db.xref="taxon:40559"
 /note="Genoscope sequence ID : W08C111"
 BASE COUNT 167 a 132 c 143 g 158 t
 ORIGIN

Query Match 88.0%; Score 13.2; DB 14; Length 600;
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RCTCCANGCRCTCCA 15
 :||||| ||:|||||
 Db 19 ACTCCAAGCACTCCA 33

RESULT 9

CNS01BUX 607 bp mRNA PLN 02-SEP-1999
 LOCUS Botrytis cinerea strain T4 cDNA library under conditions of
 nitrogen deprivation.

ACCESSION AL114721.1 GI:5829340
 VERSION cDNA library; nitrogen deprivation.
 KEYWORDS Botryotinia fuckeliana.
 SOURCE Botryotinia fuckeliana.

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
 Helotiales; Sclerotiniaceae; Botryotinia.

REFERENCE 1 (bases 1 to 607)
 AUTHORS Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.

TITLE Direct Submission
 JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
 78026 Versailles, France

REFERENCE 2 (bases 1 to 607)

Genoscope.
 Direct Submission
 Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
 CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)

COMMENT The cDNA library to be analyzed within the framework of this
 project was created using a Botrytis cinerea strain which was grown
 under conditions of nitrogen deprivation, which is the normal
 situation for B. cinerea during its development on its host plant.
 The library was produced in an oriented direction, in the pBSII
 vector.

FEATURES

source

Location/Qualifiers
 1. .607
 /organism="Botryotinia fuckeliana"
 /strain="T4"
 /db.xref="taxon:40559"
 /note="Genoscope sequence ID : W30E111"
 BASE COUNT 172 a 132 c 145 g 157 t 1 others
 ORIGIN

Query Match 88.0%; Score 13.2; DB 14; Length 607;
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGCRCTCCA 15
 :||||| ||:|||||
 Db 32 ACTCCAAGCACTCCA 46

RESULT 10

S78505/c 669 bp mRNA PRI 07-MAR-2001
 LOCUS Homo sapiens prolactin receptor mRNA, partial cds.
 DEFINITION S78505

ACCESSION S78505
 VERSION S78505.1 GI:999114
 KEYWORDS human.
 SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 669)

AUTHORS Fuh,G. and Wells,J.A.
 TITLE Prolactin receptor antagonists that inhibit the growth of breast
 cancer cell lines
 JOURNAL J. Biol. Chem. 270 (22), 13133-13137 (1995)

MEDLINE 95286597
 REMARK GenBank staff at the National Library of Medicine created this

Db 317 ACTCCATGCACTCCA 303
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RESULT 4

AR102280/c 357 bp DNA PAT 14-FEB-2001
LOCUS Sequence 3 from patent US 6083753.

DEFINITION AR102280

ACCESSION AR102280.1 GI:12813078

VERSION 1

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 357)

AUTHORS Kelly,P.A. and Nagano,M.

TITLE Soluble human prolactin receptors

JOURNAL Patent: US 6083753-A 3 04-JUL-2000;

FEATURES Location/Qualifiers

1..357

BASE COUNT 99 a 90 c 76 g 92 t

ORIGIN

Query Match 88.0%; Score 13.2; DB 9; Length 357;

Best Local Similarity 80.0%; Pred. No. 2.1e+03;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RTCCAGCGRCTCCA 15

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Db 317 ACTCCATGCACTCCA 303

RESULT 5

CNS01B4F 540 bp mRNA PLN 02-SEP-1999
LOCUS Botrytis cinerea strain T4 cDNA library under conditions of

DEFINITION nitrogen deprivation.

ACCESSION AL113767

VERSION AL113767.1 GI:5828386

KEYWORDS cDNA library; nitrogen deprivation.

SOURCE Botryotinia fuckelliana.

ORGANISM Botryotinia fuckelliana

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;

1 (bases 1 to 540)

Helotiales; Sclerotiniaceae; Botryotinia.

Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.

Direct Submission

Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,

78026 Versailles, France

2 (bases 1 to 540)

Genoscope.

Direct Submission

Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :

CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

The cDNA library to be analyzed within the framework of this

project was created using a Botrytis cinerea strain which was grown

under conditions of nitrogen deprivation, which is the normal

situation for B. cinerea during its development on its host plant.

The library was produced in an oriented direction, in the pBSII

vector.

FEATURES Location/Qualifiers

1..540

/organism="Botryotinia fuckelliana"

/strain="T4"

/db_xref="taxon:40559"

/note="Genoscope sequence ID : W24H011"

BASE COUNT 156 a 121 c 128 g 135 t

ORIGIN

Query Match

Best Local Similarity 88.0%; Score 13.2; DB 14; Length 540;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RTCCAGCGRCTCCA 15

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Db 19 ACTCCAAGCACTCCA 33

RESULT 6

CNS01D2D 540 bp mRNA PLN 03-SEP-1999
LOCUS Botrytis cinerea strain T4 cDNA library under conditions of

DEFINITION nitrogen deprivation.

ACCESSION AL116285

VERSION AL116285.1 GI:5831501

KEYWORDS cDNA library; nitrogen deprivation.

SOURCE Botryotinia fuckelliana.

ORGANISM Botryotinia fuckelliana

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;

1 (bases 1 to 540)

Helotiales; Sclerotiniaceae; Botryotinia.

Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.

Direct Submission

Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,

78026 Versailles, France

2 (bases 1 to 540)

Genoscope.

Direct Submission

Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :

CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

The cDNA library to be analyzed within the framework of this

project was created using a Botrytis cinerea strain which was grown

under conditions of nitrogen deprivation, which is the normal

situation for B. cinerea during its development on its host plant.

The library was produced in an oriented direction, in the pBSII

vector.

FEATURES Location/Qualifiers

1..540

/organism="Botryotinia fuckelliana"

/strain="T4"

/db_xref="taxon:40559"

/note="Genoscope sequence ID : W33E081"

BASE COUNT 152 a 120 c 133 g 135 t

ORIGIN

Query Match

Best Local Similarity 88.0%; Score 13.2; DB 14; Length 540;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RTCCAGCGRCTCCA 15

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Db 5 ACTCCAAGCACTCCA 19

RESULT 7

CNS018S2 600 bp mRNA PLN 02-SEP-1999
LOCUS Botrytis cinerea strain T4 cDNA library under conditions of

DEFINITION nitrogen deprivation.

ACCESSION AL110729

VERSION AL110729.1 GI:5825016

KEYWORDS cDNA library; nitrogen deprivation.

SOURCE Botryotinia fuckelliana.

ORGANISM Botryotinia fuckelliana

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;

1 (bases 1 to 600)

Helotiales; Sclerotiniaceae; Botryotinia.

Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.

Direct Submission

Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,

9 13.2 88.0 607 14 CNS01BUX
 c 10 13.2 88.0 669 97 S78505
 c 11 13.2 88.0 696 7 BOVBA2
 c 12 13.2 88.0 700 89 AF166331
 c 13 13.2 88.0 701 9 A64741
 c 14 13.2 88.0 701 94 MMU272227
 c 15 13.2 88.0 704 7 AF081273
 c 16 13.2 88.0 714 10 AX100243
 c 17 13.2 88.0 739 9 A86031
 c 18 13.2 88.0 739 10 E66049
 c 19 13.2 88.0 780 53 CNS01EU1
 c 20 13.2 88.0 912 91 BC006285
 c 21 13.2 88.0 1050 9 AR101845
 c 22 13.2 88.0 1050 9 AR102285
 c 23 13.2 88.0 1091 53 CNS060RO
 c 24 13.2 88.0 1140 9 AX010400
 c 25 13.2 88.0 1297 89 AF166329
 c 26 13.2 88.0 1448 13 ATHPROKINA
 c 27 13.2 88.0 1472 88 AF107834
 c 28 13.2 88.0 1566 89 AF349939
 c 29 13.2 88.0 1679 6 DD003413
 c 30 13.2 88.0 1681 94 MMU14412
 c 31 13.2 88.0 1713 94 AF347936
 c 32 13.2 88.0 1719 94 MMETL
 c 33 13.2 88.0 1726 94 AF131077
 c 34 13.2 88.0 1757 11 BP5FIFII
 c 35 13.2 88.0 1778 94 AF097723
 c 36 13.2 88.0 1794 89 AF119386
 c 37 13.2 88.0 1833 95 RATCALAA
 c 38 13.2 88.0 1860 9 AX006440
 c 39 13.2 88.0 1884 94 MMETL2912
 c 40 13.2 88.0 1975 94 MMU69491
 c 41 13.2 88.0 1985 94 MMU111
 c 42 13.2 88.0 2116 94 MMU72520
 c 43 13.2 88.0 2178 6 DROPOXNUP
 c 44 13.2 88.0 2213 91 BC002681
 c 45 13.2 88.0 2219 91 D89016 Homo sapien

ALIGNMENTS

RESULT 1
 A64746
 LOCUS A64746 108 bp DNA PAT 29-MAR-1999
 DEFINITION Sequence 6 from Patent W09730164.
 ACCESSION A64746
 VERSION A64746.1 GI:4530782
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 108)
 AUTHORS Haseloff, J.P. and Hodge, S.
 TITLE IMPROVEMENTS IN OR RELATING TO GENE EXPRESSION
 JOURNAL Patent: WO 9730164-A 6 21-AUG-1997;
 COMMENT MEDICAL RES COUNCIL (GB)
 FEATURES
 source 1..108
 /organism="unidentified"
 /db_xref="taxon:32644"
 BASE COUNT 18 a 25 c 46 g 19 t
 ORIGIN
 Query Match 88.0%; Score 13.2; DB 9; Length 108;
 Best Local Similarity 80.0%; Pred. No. 2.2e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RCTCCAGCGCTCCA 15
 Db 32 GCTCCAGCGCTCCA 46

RESULT 2
 HSPLR07/c
 LOCUS HSPLR07 172 bp DNA PRI 25-MAY-1999
 DEFINITION Homo sapiens prolactin receptor gene, exon 7.
 ACCESSION AF091867
 VERSION AF091867.1 GI:4886763
 KEYWORDS
 SEGMENT 7 of 10
 SOURCE human.
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 172)
 AUTHORS Hu, Z.-Z., Zhuang, L., Meng, J., Leonidires, M. and Dufau, M.L.
 TITLE The human prolactin receptor gene structure and alternative promoter utilization: the generic promoter hPRLI and a novel human promoter hP(N)
 JOURNAL J. Clin. Endocrinol. Metab. 84 (3), 1153-1156 (1999)
 MEDLINE 99182102
 PUBMED 10084611
 REFERENCE 2 (bases 1 to 172)
 AUTHORS Hu, Z.-Z., Zhuang, L., Meng, J.P. and Dufau, M.L.
 TITLE Direct Submission
 JOURNAL Submitted (16-SEP-1998) ERRB, NICHHD, 9000 Rockville Pike, Bethesda, MD 20892, USA
 FEATURES
 source 1..172
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5"
 exon 16..157
 /number=7
 BASE COUNT 44 a 43 c 39 g 46 t
 ORIGIN
 Query Match 88.0%; Score 13.2; DB 93; Length 172;
 Best Local Similarity 80.0%; Pred. No. 2.2e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RCTCCAGCGCTCCA 15
 Db 129 ACTCCATGCACTCCA 115

RESULT 3
 AR101840/c
 LOCUS AR101840 357 bp DNA PAT 14-FEB-2001
 DEFINITION Sequence 3 from patent US 6083714.
 ACCESSION AR101840
 VERSION AR101840.1 GI:12812638
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 357)
 AUTHORS Kelly, P.A. and Nagano, M.
 TITLE Soluble human prolactin receptors
 JOURNAL Patent: US 6083714-A 3 04-JUL-2000;
 FEATURES
 source 1..357
 Location/Qualifiers
 /organism="unknown"
 BASE COUNT 99 a 90 c 76 g 92 t
 ORIGIN
 Query Match 88.0%; Score 13.2; DB 9; Length 357;
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RCTCCAGCGCTCCA 15

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: August 29, 2001, 19:51:58 ; Search time 1774.1 Seconds
(without alignments)
130.780 Million cell updates/sec

Title: US-09-532-263-8
Perfect score: 15
Sequence: 1 RCTCCANGCRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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91: gb_pr7.*
92: gb_pr8.*
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94: gb_ro1.*
95: gb_ro2.*
96: gb_in4.*
97: gb_pr10.*
98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	13.2	88.0	108	9	A64746	A64746 Sequence 6
C 2	13.2	88.0	172	93	HSPLR07	AF091867 Homo sapi
C 3	13.2	88.0	357	9	AR101840	AR101840 Sequence
C 4	13.2	88.0	357	9	AR102280	AR102280 Sequence
5	13.2	88.0	540	14	CNS01B4F	AL113767 Botrytis
6	13.2	88.0	540	14	CNS01D2D	AL116285 Botrytis
7	13.2	88.0	600	14	CNS018S2	AL110729 Botrytis
8	13.2	88.0	600	14	CNS01ACZ	AL112779 Botrytis

PN US6083714-A.
 PD 04-JUL-2000.
 XX 26-FEB-1997; 97US-0806597.
 XX 29-FEB-1996; 96US-0012503.
 XX (INRM) INSRM INST NAT SANTE & RECH MEDICALE.
 PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 XX Kelly PA, Nagano M;
 PI WPI; 2000-464339/40.
 XX P-PSDB; AAY96916.
 DR New soluble prolactin receptors useful as human growth hormone binding
 PT protein and in x-ray crystallographic analysis for developing molecular
 PT models which define the tertiary structure of the hormone-binding
 PT domains
 XX Disclosure; Column 25-28; 26pp; English.

XX Soluble human prolactin receptor (hPRLR) isoforms have been isolated from
 CC the human gastrointestinal tract. The isoforms have a deletion in the
 CC extra- or intracellular domain and are thought to be generated by
 CC alternative splicing, since four clones (A, B, C and E) precisely lack
 CC one or two exons. Except for clone C, the deletion in all other clones
 CC resulted in a frameshift and produced a stop codon before the
 CC transmembrane domain. The soluble hPRLR may be used as a binding protein
 CC for human prolactin and/or human growth hormone, which can be used in
 CC diagnostics for the detection and measurement of the binding ligand or in
 CC therapeutics for binding to human prolactin and/or human growth hormone
 CC to retard or inhibit their hormone activities. They may also be used in
 CC place of monoclonal antibodies to provide solution-based radioligand
 CC receptor assays, in receptor sandwich or enzymatic assays, and in x-ray
 CC crystallographic analysis to develop molecular models, which define the
 CC tertiary structure of the hormone-binding domains, where such information
 CC would provide insight into the structure of the actual contact between a
 CC hormone and its receptor. This structural information would be useful in
 CC the design of peptides which have prolactin or growth hormone-like
 CC agonistic or antagonistic activity.
 XX Sequence 357 BP; 99 A; 90 C; 76 G; 92 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 357;
 Best Local Similarity 80.0%; Pred. NO. 3.3e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RCTCCANGCRCTCCA 15
 DB 317 ACTCCATGCACCTCCA 303

RESULT 15
 AAA49977/c
 ID AAA49977 standard; cDNA; 357 BP.
 XX AC AAA49977;
 XX 10-OCT-2000 (first entry)

XX DNA encoding soluble isoform of human prolactin receptor.
 DE Prolactin receptor; human; isoform; ss.
 XX Homo sapiens.

XX key Location/Qualifiers
 FH sig_peptide 1..72
 FT /*tag= a
 FT mat_peptide 73..354

FT /*tag= b

XX US6083753-A.
 PN 04-JUL-2000.
 XX 14-NOV-1997; 97US-0970428.
 XX 29-FEB-1996; 96US-0012503.
 PR 26-FEB-1997; 97US-0806597.
 XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 PA (INRM) INSRM INST NAT SANTE & RECH MEDICALE.
 XX Kelly PA, Nagano M;
 PI WPI; 2000-464346/40.
 XX P-PSDB; AAY95524.

XX New recombinant DNA having a segment encoding a signal peptide joined
 CC translationally to a segment encoding a soluble human prolactin
 CC receptor useful as a hormone growth hormone binding protein, and in
 CC x-ray crystallographic analysis
 XX Claim 8; Column 25-28; 27pp; English.

XX The present sequence is that of DNA encoding a newly identified
 CC soluble isoform of the human prolactin receptor (PRLR). The DNA
 CC lacks exons 5 and 6 of the full-length receptor, resulting in a
 CC frameshift that produces a stop codon before the transmembrane domain,
 CC making the putative protein product (see AAY95524) a secreted form of
 CC the receptor. 6 Isoforms (see AAA49576-82) of human PRLR were
 CC identified in human colonic Caco-2 and human breast cancer T-47D
 CC cells. Recombinant DNA molecules encoding the soluble PRLRs are
 CC provided, as well as expression vectors and host cells. The soluble
 CC PRLRs may be used as binding proteins for human prolactin and/or
 CC human growth hormone, which can be useful in diagnostics for the
 CC detection and measurement of the binding ligand, or in therapeutics
 CC for binding to human prolactin and/or human growth hormone to retard
 CC or inhibit their hormone activities. They may also be used in place
 CC of monoclonal antibodies to provide solution-based radioligand
 CC receptor assays, in receptor sandwich or enzymatic assays, and in
 CC x-ray crystallographic analysis to develop molecular models that
 CC define the tertiary structure of the hormone-binding domains, where
 CC such information would provide insight into the structure of the
 CC actual contact between a hormone and its receptor. This structural
 CC information would be useful in the design of peptides that have
 CC prolactin or growth hormone-like agonistic or antagonistic activity.

XX Sequence 357 BP; 99 A; 90 C; 76 G; 92 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 357;
 Best Local Similarity 80.0%; Pred. NO. 3.3e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RCTCCANGCRCTCCA 15
 DB 317 ACTCCATGCACCTCCA 303

Search completed: August 29, 2001, 20:16:43
 Job time: 7424 sec

```
Query Match      88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
   :||||| ||:|||||
Db 15 ACTCCATGCACCTCCA 1

RESULT 12
AAZ90895/C
ID AAZ90895 standard; DNA; 15 BP.
XX
AC AAZ90895;
XX
DT 24-MAY-2000 (first entry)
XX
DE Human NR8 gene probe #123.
XX
KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX
OS Homo sapiens.
XX
PN WO967290-A1.
XX
PD 29-DEC-1999.
XX
PF 23-JUN-1999; 99WO-JP03351.
XX
PR 24-JUN-1998; 98JP-0214720.
PR 19-OCT-1998; 98JP-0297409.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Nomura H, Maeda M;
XX
DR WPI; 2000-116933/10.
XX
PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT formation disorders.
XX
PS Example 1; Page 44; 176pp; Japanese.
XX
CC The invention relates to the isolation of sequences encoding human
CC haemopoietin receptor protein family NR8 genes. The NR8 family
CC sequences were initially searched for comparison on a nucleic acid
CC database with the nucleic acid probe sequence TGCAGYNNNTGGAGY encoding
CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
CC sequences used in the search. Antibodies to the NR8 family proteins are
CC used for the diagnosis of blood formation disorders. Compounds identified
CC as binding to the proteins are used for the treatment of such disorders.
XX
SQ Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;

Query Match      88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
   :||||| ||:|||||
Db 15 ACTCCATGCACCTCCA 1

RESULT 13
AAZ92243
ID AAZ92243 standard; DNA; 20 BP.
XX
AC AAZ92243;
XX
DT 13-SEP-1999 (first entry)
```

```
XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
DE Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; PCR primer; ss.
KW
XX Synthetic.
OS Chlamydia pneumoniae.
OS
XX WO9927105-A2.
XX
PN 03-JUN-1999.
XX
PD
XX
PF 20-NOV-1998; 98WO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae
XX Page 1496; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading
CC frames and other nucleic acid sequences from the genome of
CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC disease such as pneumonia and bronchitis and is thought to be a
CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC by the open reading frames of the C. pneumoniae genome (see AAX34584-
CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC containing C. pneumoniae nucleotide sequences can also be used as
CC immunogenic compositions, especially where the vector directs the
CC expression of a neutralising epitope of C. pneumoniae.
XX
SQ Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 other;

Query Match      88.0%; Score 13.2; DB 20; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
   :||||| ||:|||||
Db 6 gctccaagcactcca 20

RESULT 14
AAZ53588/C
ID AAZ53588 standard; cDNA; 357 BP.
XX
AC AAZ53588;
XX
DT 31-OCT-2000 (first entry)
XX
DE Soluble human prolactin receptor clone B.
XX
KW hPRLR; soluble; prolactin receptor; gastrointestinal; splice variant;
KW binding protein; prolactin; growth hormone; agonist; antagonist; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
   1..357
   /*tag= a
   /product= hPRLR_clone_B
XX
```

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XX PD 29-DEC-1999.
XX PF 23-JUN-1999; 99WO-JP03351.
XX PR 24-JUN-1998; 98JP-0214720.
XX PR 19-OCT-1998; 98JP-0297409.
XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX PI Nomura H, Maeda M;
XX DR WPI; 2000-116933/10.
XX PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
XX PT formation disorders -
XX PS Example 1; Page 42; 176pp; Japanese.
XX CC The invention relates to the isolation of sequences encoding human
XX CC haemopoietin receptor protein family NR8 genes. The NR8 family
XX CC sequences were initially searched for comparison on a nucleic acid
XX CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
XX CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
XX CC AA259258-259300 and AA290816-290925 represent specific examples of probe
XX CC sequences used in the search. Antibodies to the NR8 family proteins are
XX CC used for the diagnosis of blood formation disorders. Compounds identified
XX CC as binding to the proteins are used for the treatment of such disorders.
XX SQ Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGCGRCTCCA 15
   :||||| ||:|||||
DB 15 ACTCCAGGCACTCCA 1

RESULT 10
AAZ90877/c
ID AAZ90877 standard; DNA; 15 BP.
XX AC AAZ90877;
XX DT 24-MAY-2000 (first entry)
XX DE Human NR8 gene probe #105.
XX KW Haemopoietin receptor family; NR8; antibody; diagnosis;
XX KW blood formation disorder; fusion protein; probe; ss.
XX OS Homo sapiens.
XX PN WO9967290-A1.
XX PD 29-DEC-1999.
XX PF 23-JUN-1999; 99WO-JP03351.
XX PR 24-JUN-1998; 98JP-0214720.
XX PR 19-OCT-1998; 98JP-0297409.
XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX PI Nomura H, Maeda M;
XX DR WPI; 2000-116933/10.
XX PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
XX PT formation disorders -
XX PS Example 1; Page 42; 176pp; Japanese.
XX CC The invention relates to the isolation of sequences encoding human
XX CC haemopoietin receptor protein family NR8 genes. The NR8 family
XX CC sequences were initially searched for comparison on a nucleic acid
XX CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
XX CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
XX CC AA259258-259300 and AA290816-290925 represent specific examples of probe
XX CC sequences used in the search. Antibodies to the NR8 family proteins are
XX CC used for the diagnosis of blood formation disorders. Compounds identified
XX CC as binding to the proteins are used for the treatment of such disorders.
XX SQ Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGCGRCTCCA 15
   :||||| ||:|||||
DB 15 ACTCCAGGCACTCCA 1

RESULT 10
AAZ90877/c
ID AAZ90877 standard; DNA; 15 BP.
XX AC AAZ90877;
XX DT 24-MAY-2000 (first entry)
XX DE Human NR8 gene probe #105.
XX KW Haemopoietin receptor family; NR8; antibody; diagnosis;
XX KW blood formation disorder; fusion protein; probe; ss.
XX OS Homo sapiens.
XX PN WO9967290-A1.
XX PD 29-DEC-1999.
XX PF 23-JUN-1999; 99WO-JP03351.
XX PR 24-JUN-1998; 98JP-0214720.
XX PR 19-OCT-1998; 98JP-0297409.
XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX PI Nomura H, Maeda M;
XX DR WPI; 2000-116933/10.
XX PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
XX PT formation disorders -

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XX PS Example 1; Page 43; 176pp; Japanese.
XX CC The invention relates to the isolation of sequences encoding human
XX CC haemopoietin receptor protein family NR8 genes. The NR8 family
XX CC sequences were initially searched for comparison on a nucleic acid
XX CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
XX CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
XX CC AA259258-259300 and AA290816-290925 represent specific examples of probe
XX CC sequences used in the search. Antibodies to the NR8 family proteins are
XX CC used for the diagnosis of blood formation disorders. Compounds identified
XX CC as binding to the proteins are used for the treatment of such disorders.
XX SQ Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGCGRCTCCA 15
   :||||| ||:|||||
DB 15 ACTCCAGGCACTCCA 1

RESULT 11
AAZ90883/c
ID AAZ90883 standard; DNA; 15 BP.
XX AC AAZ90883;
XX DT 24-MAY-2000 (first entry)
XX DE Human NR8 gene probe #111.
XX KW Haemopoietin receptor family; NR8; antibody; diagnosis;
XX KW blood formation disorder; fusion protein; probe; ss.
XX OS Homo sapiens.
XX PN WO9967290-A1.
XX PD 29-DEC-1999.
XX PF 23-JUN-1999; 99WO-JP03351.
XX PR 24-JUN-1998; 98JP-0214720.
XX PR 19-OCT-1998; 98JP-0297409.
XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX PI Nomura H, Maeda M;
XX DR WPI; 2000-116933/10.
XX PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
XX PT formation disorders -
XX PS Example 1; Page 43; 176pp; Japanese.
XX CC The invention relates to the isolation of sequences encoding human
XX CC haemopoietin receptor protein family NR8 genes. The NR8 family
XX CC sequences were initially searched for comparison on a nucleic acid
XX CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
XX CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
XX CC AA259258-259300 and AA290816-290925 represent specific examples of probe
XX CC sequences used in the search. Antibodies to the NR8 family proteins are
XX CC used for the diagnosis of blood formation disorders. Compounds identified
XX CC as binding to the proteins are used for the treatment of such disorders.
XX SQ Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;

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CC sequences used in the search. Antibodies to the NR8 family proteins are
CC used for the diagnosis of blood formation disorders. Compounds identified
CC as binding to the proteins are used for the treatment of such disorders.
XX
SQ Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
:||||| ||:|||||
Db 15 ACTCCATGCACCTCCA 1

RESULT 7

AAZ90837/c
ID AAZ90837 standard; DNA; 15 BP.

XX AC AAZ90837;

XX XX 24-MAY-2000 (first entry)

XX XX Human NR8 gene probe #65.

XX KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX OS Homo sapiens.

XX XX WO9967290-A1.

XX XX 29-DEC-1999.

XX XX 23-JUN-1999; 99WO-JP03351.

XX XX 24-JUN-1998; 98JP-0214720.

XX XX 19-OCT-1998; 98JP-0297409.

XX XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX XX Nomura H, Maeda M;

XX XX WPI; 2000-116933/10.

XX KW Haemopoietin receptor protein family NR8 used for diagnosis of blood
XX formation disorders -
XX Example 1; Page 41; 176pp; Japanese.
XX The invention relates to the isolation of sequences encoding human
XX haemopoietin receptor protein family NR8 genes. The NR8 family
XX sequences were initially searched for comparison on a nucleic acid
XX database with the nucleic acid probe sequence TGCAGYNNNTGGAGY encoding
XX the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
XX AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
XX sequences used in the search. Antibodies to the NR8 family proteins are
XX used for the diagnosis of blood formation disorders. Compounds identified
XX as binding to the proteins are used for the treatment of such disorders.
XX Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
:||||| ||:|||||
Db 15 ACTCCATGCACCTCCA 1

T

RESULT 8

AAZ90861/c
ID AAZ90861 standard; DNA; 15 BP.

XX AC AAZ90861;

XX XX 24-MAY-2000 (first entry)

XX XX Human NR8 gene probe #89.

XX KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX OS Homo sapiens.

XX XX WO9967290-A1.

XX XX 29-DEC-1999.

XX XX 23-JUN-1999; 99WO-JP03351.

XX XX 24-JUN-1998; 98JP-0214720.

XX XX 19-OCT-1998; 98JP-0297409.

XX XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX XX Nomura H, Maeda M;

XX XX WPI; 2000-116933/10.

XX KW Haemopoietin receptor protein family NR8 used for diagnosis of blood
XX formation disorders -
XX Example 1; Page 42; 176pp; Japanese.
XX The invention relates to the isolation of sequences encoding human
XX haemopoietin receptor protein family NR8 genes. The NR8 family
XX sequences were initially searched for comparison on a nucleic acid
XX database with the nucleic acid probe sequence TGCAGYNNNTGGAGY encoding
XX the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
XX AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
XX sequences used in the search. Antibodies to the NR8 family proteins are
XX used for the diagnosis of blood formation disorders. Compounds identified
XX as binding to the proteins are used for the treatment of such disorders.
XX Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
:||||| ||:|||||
Db 15 ACTCCATGCACCTCCA 1

RESULT 9

AAZ90872/c
ID AAZ90872 standard; DNA; 15 BP.

XX AC AAZ90872;

XX XX 24-MAY-2000 (first entry)

XX XX Human NR8 gene probe #100.

XX KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX OS Homo sapiens.

XX XX WO9967290-A1.

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XX Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX
XX Homo sapiens.
OS
PN WO9967290-A1.
XX
XX 29-DEC-1999.
PD
XX
PF 23-JUN-1999; 99WO-JP03351.
XX
XX 24-JUN-1998; 98JP-0214720.
PR
XX 19-OCT-1998; 98JP-0297409.
PR
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PA
XX
PI Nomura H, Maeda M;
XX
XX WPI; 2000-116933/10.
XX
XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT formation disorders.
XX
XX Example 1; Page 39; 176pp; Japanese.
PS
XX The invention relates to the isolation of sequences encoding human
CC haemopoietin receptor protein family NR8 genes. The NR8 family
CC sequences were initially searched for comparison on a nucleic acid
CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
CC sequences used in the search. Antibodies to the NR8 family proteins are
CC used for the diagnosis of blood formation disorders. Compounds identified
CC as binding to the proteins are used for the treatment of such disorders.
XX
XX Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;
SQ
Query Match 88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 1 RCTCCANGCRCTCCA 15
Db :||||| ||:|||||
15 ACTCCATGCACTCCA 1
RESULT 5
AAZ90832/c
ID AAZ90832 standard; DNA; 15 BP.
XX
XX AC AAZ90832;
XX
XX 24-MAY-2000 (first entry)
DT
XX Human NR8 gene probe #60.
DE
XX Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX
XX Homo sapiens.
OS
XX WO9967290-A1.
PN
XX 29-DEC-1999.
PD
XX
XX 23-JUN-1999; 99WO-JP03351.
PF
XX
XX 24-JUN-1998; 98JP-0214720.
PR
XX 19-OCT-1998; 98JP-0297409.
PR
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PA

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XX
PI Nomura H, Maeda M;
XX
XX WPI; 2000-116933/10.
XX
XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT formation disorders.
XX
XX Example 1; Page 40; 176pp; Japanese.
PS
XX The invention relates to the isolation of sequences encoding human
CC haemopoietin receptor protein family NR8 genes. The NR8 family
CC sequences were initially searched for comparison on a nucleic acid
CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
CC sequences used in the search. Antibodies to the NR8 family proteins are
CC used for the diagnosis of blood formation disorders. Compounds identified
CC as binding to the proteins are used for the treatment of such disorders.
XX
XX Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;
SQ
Query Match 88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 1 RCTCCANGCRCTCCA 15
Db :||||| ||:|||||
15 ACTCCAGCACTCCA 1
RESULT 6
AAZ90836/c
ID AAZ90836 standard; DNA; 15 BP.
XX
XX AC AAZ90836;
XX
XX 24-MAY-2000 (first entry)
DT
XX Human NR8 gene probe #64.
DE
XX Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX
XX Homo sapiens.
OS
XX WO9967290-A1.
PN
XX 29-DEC-1999.
PD
XX
XX 23-JUN-1999; 99WO-JP03351.
PF
XX
XX 24-JUN-1998; 98JP-0214720.
PR
XX 19-OCT-1998; 98JP-0297409.
PR
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PA
XX
XX Nomura H, Maeda M;
XX
XX WPI; 2000-116933/10.
XX
XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT formation disorders.
XX
XX Example 1; Page 40; 176pp; Japanese.
PS
XX The invention relates to the isolation of sequences encoding human
CC haemopoietin receptor protein family NR8 genes. The NR8 family
CC sequences were initially searched for comparison on a nucleic acid
CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
CC sequences used in the search. Antibodies to the NR8 family proteins are
CC used for the diagnosis of blood formation disorders. Compounds identified
CC as binding to the proteins are used for the treatment of such disorders.
XX
XX Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;
SQ

```

XX The invention relates to the isolation of sequences encoding human
 CC haemopoietin receptor protein family NR8 genes. The NR8 family
 CC sequences were initially searched for comparison on a nucleic acid
 CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
 CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 CC AAZ5258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
 CC sequences used in the search. Antibodies to the NR8 family proteins are
 CC used for the diagnosis of blood formation disorders. Compounds identified
 CC as binding to the proteins are used for the treatment of such disorders.
 XX
 SQ Sequence 15 BP; 2 A; 3 C; 7 G; 3 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;

Best Local Similarity 80.0%; Pred. No. 2.6e+02;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
 :||||| ||:|||||
 Db 15 GCTCCAGGCACTCCA 1

RESULT 2

AAZ59267/c

ID AAZ59267 standard; DNA; 15 BP.

XX AAZ59267;

XX 24-MAY-2000 (first entry)

XX Human NR8 gene probe #10.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;

XX blood formation disorder; fusion protein; probe; ss.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood

XX formation disorders -

XX Example 1; Page 38; 176pp; Japanese.

XX The invention relates to the isolation of sequences encoding human

XX haemopoietin receptor protein family NR8 genes. The NR8 family

XX sequences were initially searched for comparison on a nucleic acid

XX database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding

XX the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences

XX AAZ5258-Z59300 and AAZ90816-Z90925 represent specific examples of probe

XX sequences used in the search. Antibodies to the NR8 family proteins are

XX used for the diagnosis of blood formation disorders. Compounds identified

XX as binding to the proteins are used for the treatment of such disorders.

XX Sequence 15 BP; 2 A; 2 C; 7 G; 4 T; 0 other;

XX Query Match 88.0%; Score 13.2; DB 21; Length 15;

XX Best Local Similarity 80.0%; Pred. No. 2.6e+02;

XX Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

XX QY 1 RCTCCANGCRCTCCA 15

XX :||||| ||:|||||

XX Db 15 ACTCCATGCCTCCA 1

XX RESULT 4

XX AAZ59282/c

XX ID AAZ59282 standard; DNA; 15 BP.

XX AAZ59282;

XX 24-MAY-2000 (first entry)

XX Human NR8 gene probe #25.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15

:||||| ||:|||||

Db 15 ACTCCAGGCACTCCA 1

RESULT 3

AAZ59278/c

ID AAZ59278 standard; DNA; 15 BP.

XX AAZ59278;

XX 24-MAY-2000 (first entry)

XX Human NR8 gene probe #21.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;

XX blood formation disorder; fusion protein; probe; ss.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood

XX formation disorders -

XX Example 1; Page 38; 176pp; Japanese.

XX The invention relates to the isolation of sequences encoding human

XX haemopoietin receptor protein family NR8 genes. The NR8 family

XX sequences were initially searched for comparison on a nucleic acid

XX database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding

XX the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences

XX AAZ5258-Z59300 and AAZ90816-Z90925 represent specific examples of probe

XX sequences used in the search. Antibodies to the NR8 family proteins are

XX used for the diagnosis of blood formation disorders. Compounds identified

XX as binding to the proteins are used for the treatment of such disorders.

XX Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;

XX Query Match 88.0%; Score 13.2; DB 21; Length 15;

XX Best Local Similarity 80.0%; Pred. No. 2.6e+02;

XX Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

XX QY 1 RCTCCANGCRCTCCA 15

XX :||||| ||:|||||

XX Db 15 ACTCCATGCCTCCA 1

XX RESULT 4

XX AAZ59282/c

XX ID AAZ59282 standard; DNA; 15 BP.

XX AAZ59282;

XX 24-MAY-2000 (first entry)

XX Human NR8 gene probe #25.

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 20:16:42 ; Search time 301.32 Seconds
(without alignments)
31.258 Million cell updates/sec

Title: US-09-532-263-8
Perfect score: 15
Sequence: 1 RCTCCANGCRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues 1460202
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :		N_Geneseq_0601.*	
1:	/SID88/gcgdata/geneseq/geneseqn/NA1980.DAT.*	2:	/SID88/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3:	/SID88/gcgdata/geneseq/geneseqn/NA1982.DAT.*	4:	/SID88/gcgdata/geneseq/geneseqn/NA1983.DAT.*
5:	/SID88/gcgdata/geneseq/geneseqn/NA1984.DAT.*	6:	/SID88/gcgdata/geneseq/geneseqn/NA1985.DAT.*
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11:	/SID88/gcgdata/geneseq/geneseqn/NA1990.DAT.*	12:	/SID88/gcgdata/geneseq/geneseqn/NA1991.DAT.*
13:	/SID88/gcgdata/geneseq/geneseqn/NA1992.DAT.*	14:	/SID88/gcgdata/geneseq/geneseqn/NA1993.DAT.*
15:	/SID88/gcgdata/geneseq/geneseqn/NA1994.DAT.*	16:	/SID88/gcgdata/geneseq/geneseqn/NA1995.DAT.*
17:	/SID88/gcgdata/geneseq/geneseqn/NA1996.DAT.*	18:	/SID88/gcgdata/geneseq/geneseqn/NA1997.DAT.*
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21:	/SID88/gcgdata/geneseq/geneseqn/NA2000.DAT.*	22:	/SID88/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
C 1	13.2	88.0	15	21	AAZ59263		Human NR8 gene pro
C 2	13.2	88.0	15	21	AAZ59267		Human NR8 gene pro
C 3	13.2	88.0	15	21	AAZ59278		Human NR8 gene pro
C 4	13.2	88.0	15	21	AAZ59282		Human NR8 gene pro
C 5	13.2	88.0	15	21	AAZ90832		Human NR8 gene pro
C 6	13.2	88.0	15	21	AAZ90836		Human NR8 gene pro
C 7	13.2	88.0	15	21	AAZ90837		Human NR8 gene pro
C 8	13.2	88.0	15	21	AAZ90861		Human NR8 gene pro
C 9	13.2	88.0	15	21	AAZ90872		Human NR8 gene pro
C 10	13.2	88.0	15	21	AAZ90877		Human NR8 gene pro
C 11	13.2	88.0	15	21	AAZ90883		Human NR8 gene pro

C 12	13.2	88.0	15	21	AAZ90895	Human NR8 gene pro
C 13	13.2	88.0	20	20	AAZ92243	PCR primer used to
C 14	13.2	88.0	357	21	AAZ53588	Soluble human prol
C 15	13.2	88.0	357	21	AAZ9977	DNA encoding solub
C 16	13.2	88.0	555	20	AAV90098	EST clone CW1682.
C 17	13.2	88.0	701	18	AAZ94500	GAL4 DNA binding d
C 18	13.2	88.0	714	22	AAZ85557	CNA encoding CDIF
C 19	13.2	88.0	825	12	AAQ11855	Glutamate receptor
C 20	13.2	88.0	1050	21	AAZ53593	Soluble human prol
C 21	13.2	88.0	1050	21	AAZ9980	DNA encoding novel
C 22	13.2	88.0	1134	21	AAZ98101	Human secreted pro
C 23	13.2	88.0	1140	21	AAZ40400	Murine soluble int
C 24	13.2	88.0	1448	22	AAF31051	Protein kinase cod
C 25	13.2	88.0	1705	17	AAZ17868	Murine Interleukin
C 26	13.2	88.0	1714	17	AAZ32613	Murine Etl-2 gene.
C 27	13.2	88.0	1767	21	AAZ40493	Human fetal kidney
C 28	13.2	88.0	1778	18	AAV02296	Human secreted pro
C 29	13.2	88.0	1851	19	AAV82779	Clone bu45_2 isola
C 30	13.2	88.0	1863	21	AAZ98034	Human secreted pro
C 31	13.2	88.0	1884	21	AAZ58313	Human peptidase NA
C 32	13.2	88.0	1899	13	AAQ24321	Mutant thermostabl
C 33	13.2	88.0	1923	21	AAZ98139	Human signal pepti
C 34	13.2	88.0	2043	13	AAQ24320	Mutant thermostabl
C 35	13.2	88.0	2172	19	AAV02996	Mammalian Ena (Men
C 36	13.2	88.0	2277	13	AAQ24013	Mutant thermostabl
C 37	13.2	88.0	2370	13	AAQ24012	Mutant thermostabl
C 38	13.2	88.0	2505	13	AAQ24011	Mutant thermostabl
C 39	13.2	88.0	2690	20	AAZ20208	Sugarbeet raffinose
C 40	13.2	88.0	2723	12	AAQ10550	Human prolactin re
C 41	13.2	88.0	2898	19	AAV02998	Mouse neural Mena+
C 42	13.2	88.0	143068	21	AAF21105	Human low adenosin
C 43	13.2	88.0	143068	21	AAF21272	Human low adenosin
C 44	13.2	88.0	143068	21	AAA34983	Human adenosine re
C 45	13.2	88.0	143068	21	AAA35150	Human adenosine re

ALIGNMENTS

RESULT 1	AAZ59263/c
ID	AAZ59263 standard; DNA; 15 BP.
XX	XX
AC	AAZ59263;
XX	XX
DT	24-MAY-2000 (first entry)
XX	XX
DE	Human NR8 gene probe #6.
XX	XX
KW	Haemopoietin receptor family; NR8; antibody; diagnosis;
XX	XX
OS	Homo sapiens.
PN	WO9967290-A1.
XX	XX
PD	29-DEC-1999.
XX	XX
PF	23-JUN-1999; 99WO-JP03351.
XX	XX
PR	24-JUN-1998; 98JP-0214720.
XX	XX
PR	19-OCT-1998; 98JP-0297409.
XX	XX
PA	(CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX	XX
PI	Nomura H, Maeda M;
XX	XX
DR	WPI; 2000-116933/10.
XX	XX
PT	Hemopoietin receptor protein family NR8 used for diagnosis of blood
XX	XX
PT	formation disorders -
XX	XX
PS	Example 1; Page 38; 176pp; Japanese.

Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tomimaga,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

TITLE
JOURNAL
COMMENT

RIKEN Mouse ESTS
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp

Thermal stabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.

FEATURES
source

Location/Qualifiers
1..175
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2200005J24"
/clone_lib="Mus musculus stomach C57BL/6J adult"
/sex="male"
/tissue_type="stomach"
/dev_stage="adult"

BASE COUNT 44 a 54 c 32 g 45 t
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Query Match 88.0%; Score 13.2; DB 109; Length 175;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGCGCTCCA 15
Db :|||||:|||||
57 ACTCCAGCGCTCCA 71

RESULT 15
AV081754

LOCUS AV081754 177 bp mRNA EST 25-JUN-1999
DEFINITION AV081754 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
clone 2210421D01, mRNA sequence.

ACCESSION AV081754
VERSION AV081754.1 GI:5213202

KEYWORDS EST.
SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
A., Hayatsu,N., Horii,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tomimaga,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

TITLE
JOURNAL
COMMENT

RIKEN Mouse ESTS
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp

Thermal stabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.

FEATURES
source

Location/Qualifiers
1..177
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2210421D01"
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/sex="male"
/tissue_type="stomach"
/dev_stage="adult"

BASE COUNT 38 a 61 c 35 g 43 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 109; Length 177;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGCGCTCCA 15
Db :|||||:|||||
58 ACTCCAGCGCTCCA 72

Search completed: August 29, 2001, 19:22:14
Job time: 24137 sec

Query Match 88.0%; Score 13.2; DB 109; Length 171;
 Best Local Similarity 80.0%; Pred. No. 4.8e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCCTCCA 15
 :||||| ||:|||||
 Db 53 ACTCCAGCGCTCCA 67

RESULT 12
 AV072886 173 bp mRNA EST 24-JUN-1999
 LOCUS AV072886 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
 DEFINITION clone 2200007C09, mRNA sequence.

ACCESSION AV072886
 VERSION AV072886
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 173)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
 Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
 A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
 Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
 Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
 Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
 Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
 Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs
 JOURNAL Unpublished (1999)
 COMMENT Contact: Chile Owa
 Genome Science Laboratory

RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098

Email: genome-res@rtc.riken.go.jp
 Thermostabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length cDNA
 (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES Location/Qualifiers
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 /sex="male"
 /tissue_type="stomach"
 /dev_stage="adult"
 BASE COUNT 38 a 58 c 46 t 1 others
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Query Match 88.0%; Score 13.2; DB 109; Length 173;
 Best Local Similarity 80.0%; Pred. No. 4.8e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCCTCCA 15
 :||||| ||:|||||
 Db 55 ACTCCAGCGCTCCA 69

RESULT 13
 AV072630 174 bp mRNA EST 24-JUN-1999
 LOCUS AV072630 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
 DEFINITION clone 2200005J24, mRNA sequence.

clone 2200005H20, mRNA sequence.

ACCESSION AV072630
 VERSION AV072630.1 GI:5192458
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 174)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
 Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
 A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
 Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
 Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
 Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
 Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
 Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs
 JOURNAL Unpublished (1999)
 COMMENT Contact: Chile Owa
 Genome Science Laboratory

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 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
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 trehalose and its application for the synthesis of full length cDNA
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 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES Location/Qualifiers
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 /organism="Mus musculus"
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 /clone="2200005H20"
 /clone_lib="Mus musculus stomach C57BL/6J adult"
 /sex="male"
 /tissue_type="stomach"
 /dev_stage="adult"
 BASE COUNT 46 a 49 c 28 g 50 t 1 others
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Query Match 88.0%; Score 13.2; DB 109; Length 174;
 Best Local Similarity 80.0%; Pred. No. 4.8e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCCTCCA 15
 :||||| ||:|||||
 Db 56 ACTCCAGCGCTCCA 70

RESULT 14
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 LOCUS AV072658 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
 DEFINITION clone 2200005J24, mRNA sequence.

ACCESSION AV072658
 VERSION AV072658.1 GI:5192486
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 175)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
 Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
 A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
 Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-cold, Tl-resistant, F-"
 /note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-cold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 26 a 36 c 56 g 46 t
 ORIGIN

Query Match 88.0%; Score 13.2; DB 242; Length 164;
 Best Local Similarity 80.0%; Pred. No. 4.8e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
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 Db 62 ACTCCAGGCCTCCA 48

RESULT 10
 AV073140
 LOCUS
 DEFINITION AV073140 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
 clone 2200008009, mRNA sequence.
 ACCESSION AV073140
 VERSION AV073140.1 GI:5192968
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 166)
 Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
 Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
 ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
 Kikuchi,N., Kojima,Y., Matsuyama,T., Niltsuma,H., Oda,H., Owa,C.,
 Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
 ,Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y., Tominaga,N.,
 Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
 Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

TITLE
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 Thermotabilization and thermoactivation of thermostable enzymes by
 trehalose and its application for the synthesis of full length cDNA
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 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES
 Location/Qualifiers

source

1. .166
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="Mus musculus stomach C57BL/6J adult"
 /sex="male"
 /tissue_type="stomach"
 /dev_stage="adult"
 BASE COUNT 34 a 49 c 33 g 47 t 3 others
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Query Match 88.0%; Score 13.2; DB 109; Length 166;
 Best Local Similarity 80.0%; Pred. No. 4.8e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
 :||||| ||:|||||
 Db 18 ACTCCAGGCCTCCA 32

RESULT 11
 AV076989
 LOCUS
 DEFINITION AV076989 171 bp mRNA EST 24-JUN-1999
 clone 2210021D15, mRNA sequence.
 ACCESSION AV076989
 VERSION AV076989.1 GI:5196817
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 171)
 Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
 Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
 ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
 Kikuchi,N., Kojima,Y., Matsuyama,T., Niltsuma,H., Oda,H., Owa,C.,
 Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
 ,Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y., Tominaga,N.,
 Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
 Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

TITLE
 JOURNAL
 COMMENT
 Unpublished (1999)
 Contact: Chie Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@rtc.riken.go.jp
 Thermotabilization and thermoactivation of thermostable enzymes by
 trehalose and its application for the synthesis of full length cDNA
 (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES
 Location/Qualifiers

source

1. .171
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="2210021D15"
 /clone_lib="Mus musculus stomach C57BL/6J adult"
 /sex="male"
 /tissue_type="stomach"
 /dev_stage="adult"
 BASE COUNT 39 a 53 c 32 g 47 t
 ORIGIN

FEATURES

Location/Qualifiers

Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagane,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

TITLE JOURNAL COMMENT

RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

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Thermotabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES source

1. .162
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="2200006408"
/clone_lib="Mus musculus stomach C57BL/6J adult"
/sex="male"
/tissue_type="stomach"
/dev_stage="adult"

BASE COUNT 34 a 50 c 30 g 48 t

Query Match 88.0%; Score 13.2; DB 109; Length 162;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
:||||| ||:|||||
DB 44 ACTCCAGCGCTCCA 58

RESULT 8

BE069562 162 bp mRNA EST 09-JUN-2000
LOCUS RC2-BT0389-090300-012-f12 BT0389 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE069562
ACCESSION BE069562.1 GI:84114212
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162)
Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.K., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC2-BT0389-090300-012-f126t3-2000-03-096t4-1)
300-012-f126t3-2000-03-096t4-1)
Seq primer: puc 18 forward
High quality sequence start: 44
High quality sequence stop: 162.

FEATURES source

1. .162
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0389"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site.1: SmaI; Site.2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 51 a 33 c 37 g 41 t

Query Match 88.0%; Score 13.2; DB 163; Length 162;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGCRCTCCA 15
:||||| ||:|||||
DB 71 GCTCCATGCACCTCCA 85

RESULT 9

AZ376266/c 164 bp DNA GSS 02-OCT-2000
LOCUS 1M0130J06F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0130J06 F, DNA sequence.
DEFINITION AZ376266
ACCESSION AZ376266.1 GI:10489966
VERSION GSS.
KEYWORDS house mouse.
SOURCE Mus musculus

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 164)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0130 row: J column: 06
Seq primer: CGTTGTAACGACGCCACT

Class: plasmid ends
High quality sequence stop: 164.

Location/Qualifiers

1. .164
/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIM0130J06"

FEATURES source

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Query Match      88.0%; Score 13.2; DB 109; Length 159;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTCCANGCRCTCCA 15
   :||||| :|:|||||
Db 47 ACTCCAGGCGCTCCA 61

RESULT 5
AV074451
LOCUS      160 bp mRNA EST 24-JUN-1999
DEFINITION Mus musculus stomach C57BL/6J adult Mus musculus cDNA
clone 2210009E18, mRNA sequence.
ACCESSION AV074451
VERSION    AV074451
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 160)
AUTHORS    Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
,Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y., Tomimaga,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
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trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES             Location/Qualifiers
     source           1..160
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2210009E18"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
BASE COUNT      35 a 49 c 29 g 47 t
ORIGIN
Query Match      88.0%; Score 13.2; DB 109; Length 160;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTCCANGCRCTCCA 15
   :||||| :|:|||||
Db 42 ACTCCAGGCGCTCCA 56

RESULT 6
AV074715
LOCUS      161 bp mRNA EST 24-JUN-1999
DEFINITION Mus musculus stomach C57BL/6J adult Mus musculus cDNA
clone 220006M08, mRNA sequence.
ACCESSION AV072831
VERSION    AV072831
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 162)
AUTHORS    Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
,Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y., Tomimaga,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
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trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES             Location/Qualifiers
     source           1..161
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2210010H07"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
BASE COUNT      36 a 42 c 32 g 49 t 2 others
ORIGIN
Query Match      88.0%; Score 13.2; DB 109; Length 161;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RTCCANGCRCTCCA 15
   :||||| :|:|||||
Db 42 ACTCCAGGCGCTCCA 56

RESULT 7
AV072831
LOCUS      162 bp mRNA EST 24-JUN-1999
DEFINITION Mus musculus stomach C57BL/6J adult Mus musculus cDNA
clone 220006M08, mRNA sequence.
ACCESSION AV072831
VERSION    AV072831
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 162)
AUTHORS    Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
,Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y., Tomimaga,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
RIKEN Mouse ESTs
Unpublished (1999)
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Email: genome-res@rtc.riken.go.jp
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(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES             Location/Qualifiers
     source           1..161
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2210010H07"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
BASE COUNT      36 a 42 c 32 g 49 t 2 others
ORIGIN

```

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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

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FEATURES

source

Location/Qualifiers

1. .135

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="2210413F10"

/clone_lib="Mus musculus stomach C57BL/6J adult"

/sex="male"

/tissue_type="stomach"

/dev_stage="adult"

26 a 41 C 26 g 42 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 13.2; DB 109; Length 135;
 Best Local Similarity 80.0%; Pred. No. 4.7e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RCTCCANGCRCTCCA 15

:||||| ||:|||||

Db 16 ACTCCAGGCGCTCCA 30

RESULT 3

AV081442

LOCUS

DEFINITION AV081442 Mus musculus stomach C57BL/6J adult Mus musculus cDNA

Accession AV081442

Version AV081442.1 GI:5212890

Keywords EST.

Source house mouse.

Organism Mus musculus

Reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Authors Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 137)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,

Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara

A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,

Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,

Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara

Y., Suzuki, H., Suzuki, H., Tatenno, M., Tomaru, Y., Tomimaga, N.,

Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,

Muranatsu, M., Okazaki, Y. and Hayashizaki, Y.

Unpublished (1999)

Contact: Chie Owa

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(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

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further details.

FEATURES

source

Location/Qualifiers

1. .137

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="2210419B03"

/clone_lib="Mus musculus stomach C57BL/6J adult"

/sex="male"

/tissue_type="stomach"

/dev_stage="adult"

29 a 41 C 27 g 40 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 13.2; DB 109; Length 137;
 Best Local Similarity 80.0%; Pred. No. 4.7e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RCTCCANGCRCTCCA 15

:||||| ||:|||||

Db 20 ACTCCAGGCGCTCCA 34

RESULT 4

AV072952

LOCUS

DEFINITION AV072952 Mus musculus stomach C57BL/6J adult Mus musculus cDNA

Accession AV072952

Version AV072952.1 GI:5192780

Keywords EST.

Source house mouse.

Organism Mus musculus

Reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Authors Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 159)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,

Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara

A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,

Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,

Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara

Y., Suzuki, H., Suzuki, H., Tatenno, M., Tomaru, Y., Tomimaga, N.,

Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,

Muranatsu, M., Okazaki, Y. and Hayashizaki, Y.

Unpublished (1999)

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Tel: 81-298-36-9145

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trehalose and its application for the synthesis of full length cDNA

(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

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further details.

Location/Qualifiers

1. .159

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="2200007101"

/clone_lib="Mus musculus stomach C57BL/6J adult"

/sex="male"

/tissue_type="stomach"

/dev_stage="adult"

34 a 51 C 27 g 46 t

BASE COUNT

ORIGIN

1 others

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	13.2	88.0	119	155	BG607593	WHE2480_H
2	13.2	88.0	135	109	AV080202	AV080202
3	13.2	88.0	137	109	AV081442	AV081442
4	13.2	88.0	159	109	AV072952	AV072952
5	13.2	88.0	160	109	AV074451	AV074451
6	13.2	88.0	161	109	AV074715	AV074715
7	13.2	88.0	162	109	AV072831	AV072831
8	13.2	88.0	163	109	BE069562	RC2-ET038
9	13.2	88.0	164	242	AZ376266	AV072658
10	13.2	88.0	166	109	AV073140	AV073140
11	13.2	88.0	171	109	AV076989	AV076989
12	13.2	88.0	173	109	AV072886	AV072886
13	13.2	88.0	174	109	AV072630	AV072630
14	13.2	88.0	175	109	AV072658	AV072658
15	13.2	88.0	177	109	AV081754	AV081754
16	13.2	88.0	179	109	AV058439	AV058439
17	13.2	88.0	179	219	CNS00TGF	Arabidops
18	13.2	88.0	180	109	AV077479	AV077479
19	13.2	88.0	190	109	AV072558	AV072558
20	13.2	88.0	191	109	AV077821	AV077821
21	13.2	88.0	192	109	AV073191	AV073191
22	13.2	88.0	192	109	AV077830	AV077830
23	13.2	88.0	192	145	BF145876	WHE1833_F
24	13.2	88.0	194	109	AV072580	AV072580
25	13.2	88.0	194	109	AV072872	AV072872
26	13.2	88.0	195	109	AV088929	AV088929
27	13.2	88.0	200	109	AV072772	AV072772
28	13.2	88.0	202	109	AV072097	AV072097
29	13.2	88.0	205	109	AV073900	AV073900
30	13.2	88.0	205	109	AV077817	AV077817
31	13.2	88.0	209	12	AA840811	CFB32 Flo
32	13.2	88.0	211	174	BG141411	la38q01.Y
33	13.2	88.0	217	138	BE670421	7e34H01.X
34	13.2	88.0	223	109	AV072887	AV072887
35	13.2	88.0	224	109	AV072779	AV072779
36	13.2	88.0	227	109	AV072787	AV072787
37	13.2	88.0	229	109	AV072799	AV072799
38	13.2	88.0	231	109	AV074114	AV074114
39	13.2	88.0	234	109	AV072750	AV072750
40	13.2	88.0	240	5	AA313785	EST22073
41	13.2	88.0	240	107	AU071883	AU071883
42	13.2	88.0	241	28	AV288598	AV288598
43	13.2	88.0	243	22	AI618724	zwp0296
44	13.2	88.0	252	109	AV077480	AV077480
45	13.2	88.0	255	109	AV078355	AV078355

ALIGNMENTS

RESULT 1	BG607593	119 bp	mRNA	EST	17-APR-2001
LOCUS	WHE2480_H02_0042s	Triticum monococcum	early reproductive apex	cDNA	
DEFINITION	Library Triticum monococcum cDNA clone WHE2480_H02_004			mRNA	
ACCESSION	BG607593.1	GI:13657576			
VERSION	EST.				
KEYWORDS	Triticum monococcum				
SOURCE	Triticum monococcum				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
REFERENCE	1 (bases 1 to 119)				
AUTHORS	Anderson, O.D., Chao, S., Dubcovsky, J., Echenique, V., Han, P.S., Hsia				
	, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L.,				

TITLE

JOURNAL COMMENT

Stamova, B. and Tong, J.C.
The structure and function of the expressed portion of the wheat
genomes - Early reproductive apex cDNA library from Triticum
monococcum
Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.

FEATURES source

Location/Qualifiers
1..119
/organism="Triticum monococcum"
/cultivar="DV92"
/db_xref="taxon:4568"
/clone="WHE2480_H02_004"
cDNA library
/tissue_type="Early reproductive apex"
/dev_stage="Seven week-old plants"
/lab_host="E. coli XL0Lp"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; The tissue, total RNA, and
poly(A) RNA were prepared from apex at double-ridge stage
to terminal-spikelet stage during transition from
vegetative state to flower state, a cDNA library was made,
and the cDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
, J. Dubcovsky). Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."

BASE COUNT 13 a 47 c 46 g 13 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 155; Length 119;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCAGCCTCCA 15
:||||| ||:|||||
Db 69 GCTCCATGCACTCCA 83

RESULT 2
AV080202 135 bp mRNA EST 25-JUN-1999
LOCUS AV080202 Mus musculus stomach C57BL/6J adult Mus musculus CDNA
clone 2210413F10, mRNA sequence.
ACCESSION AV080202
VERSION AV080202.1 GI:5211650
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 135)
AUTHORS Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara
, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsuma, H., Oda, H., Owa, C.,
Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara
, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N.,
Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
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256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:22:13 ; Search time 3770.35 seconds
(without alignments)
37.607 Million cell updates/sec

Title: US-09-532-263-8

Perfect score: 15

Sequence: 1 RCTCCANGCRCTCCA 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4736426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

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4: gb_est4.*
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1. 445
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/note="exon 1"
268. .>534
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/codon_start=1
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/protein_id="CAA39921.1"
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/db_xref="MGD:MGI:97857"
/db_xref="SWISS-PROT:P22605"
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mat_peptide
119 a 165 c 135 g 115 t
BASE COUNT
ORIGIN

Query Match 88.0%; Score 13.2; DB 94; Length 534;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGCTCCA 15
:||||| ||:|||||
Db 387 ACTCCATGGGCTCCA 401

RESULT 15
MMU276872/c 573 bp mRNA ROD 02-FEB-2001
LOCUS Mus musculus mRNA for GDNF family receptor alpha 4, putative
DEFINITION secreted isoform (Gfra4 gene).
ACCESSION AJ276872
VERSION AJ276872.1 GI:7688070
KEYWORDS alternative splicing; GDNF family receptor alpha 4; Gfra4 gene.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 573)
Lindahl, M., Timmusk, T., Rossi, J., Saarma, M. and Airaksinen, M. S.
Expression and alternative splicing of mouse Gfra4 suggest roles in
endocrine cell development
Mol. Cell. Neurosci. 15 (6), 522-533 (2000)
20319126
2 (bases 1 to 573)
Airaksinen, M. S.
Direct Submission
Submitted (20-MAR-2000) Airaksinen M. S., Program in Molecular
Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari
9), 00014 University of Helsinki, FINLAND
Location/Qualifiers
1. 573
/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="thyroid"
1. 573.
/gene="Gfra4"
1. 573

gene
CDS

/gene="Gfra4"
/note="transcript a3/a4 produced by inclusion of the short
53 bp intron separating exons II and III"
/codon_start=1
/product="putative GDNF family receptor alpha 4, secreted
isoform"
/protein_id="CAB89692.1"
/db_xref="GI:7688071"
/db_xref="SPTREMBL:Q9JJT2"
/translation="NAHWESALLLLLLLGSASFDTGNCVDAEACTADRCQQLRS
EYVARCLGRAAPGGPGGCVSRRCRRALRRFFARGPPALHLLFCGCEGSACAER
RRQTPAPACAFSGPLVPPSCLEPLERCERSRLRCVRAGRAGPLTRRARAGPVSLP
SRPHALPRPAPATAARRRGARVVCASTQAS"

BASE COUNT 49 a 213 c 215 g 96 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 94; Length 573;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGCTCCA 15
:||||| ||:|||||
Db 385 GCTCCAGGGGCTCCA 371

Search completed: August 29, 2001, 19:52:01
Job time: 17239 sec

SOURCE
ORGANISM Echinometra mathaei.
 Mitochondrion Echinometra mathaei
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
 Echinometra.

REFERENCE
AUTHORS 1 (bases 1 to 450)
TITLE Palumbi,S.R., Grabowski,G., Duda,T., Geyer,L. and Tachino,N.
 Speciation and population genetic structure in tropical Pacific sea
 urchins

JOURNAL Evolution 51 (5), 1506-1517 (1997)

REFERENCE
AUTHORS 2 (bases 1 to 450)
TITLE Palumbi,S.R., Grabowski,G., Duda,T., Geyer,L. and Tachino,N.
 Direct Submission

JOURNAL Submitted (12-AUG-1997) OEB, Harvard University, 16 Divinity
 Avenue, Cambridge, MA 02138, USA

FEATURES
 Location/Qualifiers
 1..450
 /organism="Echinometra mathaei"
 /organelle="mitochondrion"
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 GVLVAHMFMTVMQVDTRAXXAATMILAVPTGIKVFSSMAXLOGNSLOWETPLFWA
 LGVFVLTGLGLTGIVLANSIDVLDHYVVAHFHYXMGAVFAI"
 BASE COUNT 117 a 103 c 93 g 125 t 12 others
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Query Match 88.0%; Score 13.2; DB 5; Length 450;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGRCCTCCA 15 STS 31-DEC-1997
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 Db 137 ACTCCAAGGACTCCA 123

RESULT 13
G36845
LOCUS G36845 477 bp DNA STS
DEFINITION SHGC-60507 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G36845
VERSION G36845.1 GI:2734512
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 477)
TITLE Myers,R.M.
JOURNAL Human STSs (1997)
COMMENT Unpublished (1997)
 Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 4157259687
 Fax: 4157259689
 Email: myers@shgc.stanford.edu
 Primer A: GGTGCGACAGACAGATTGTG
 Primer B: ATGCACATGAAGCATGGAG
 STS size: 205
 PCR Profile:
 Initial incubation: 95 degrees C for 10 minutes
 Denaturation: 94 degrees C for 30 seconds

SOURCE
ORGANISM Echinometra mathaei.
 Mitochondrion Echinometra mathaei
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
 Echinometra.

REFERENCE
AUTHORS 1 (bases 1 to 450)
TITLE Palumbi,S.R., Grabowski,G., Duda,T., Geyer,L. and Tachino,N.
 Speciation and population genetic structure in tropical Pacific sea
 urchins

JOURNAL Evolution 51 (5), 1506-1517 (1997)

REFERENCE
AUTHORS 2 (bases 1 to 450)
TITLE Palumbi,S.R., Grabowski,G., Duda,T., Geyer,L. and Tachino,N.
 Direct Submission

JOURNAL Submitted (12-AUG-1997) OEB, Harvard University, 16 Divinity
 Avenue, Cambridge, MA 02138, USA

FEATURES
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 /organelle="mitochondrion"
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 /protein_id="AAB69575.1"
 /db_xref="GI:2353672"
 /translation="HPEVYILILPGFMISHVIAHSGKREPGLGMVYAMIAIGVL
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 LGVFVLTGLGLTGIVLANSIDVLDHYVVAHFHYXMGAVFAI"
 BASE COUNT 117 a 103 c 93 g 125 t 12 others
 ORIGIN

Query Match 88.0%; Score 13.2; DB 5; Length 450;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGRCCTCCA 15 STS 31-DEC-1997
 :||||| ||:|||||
 Db 137 ACTCCAAGGACTCCA 123

RESULT 13
G36845
LOCUS G36845 477 bp DNA STS
DEFINITION SHGC-60507 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G36845
VERSION G36845.1 GI:2734512
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 477)
TITLE Myers,R.M.
JOURNAL Human STSs (1997)
COMMENT Unpublished (1997)
 Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 4157259687
 Fax: 4157259689
 Email: myers@shgc.stanford.edu
 Primer A: GGTGCGACAGACAGATTGTG
 Primer B: ATGCACATGAAGCATGGAG
 STS size: 205
 PCR Profile:
 Initial incubation: 95 degrees C for 10 minutes
 Denaturation: 94 degrees C for 30 seconds

Annealing: 60 degrees C for 30 seconds
 Polymerization: 72 degrees C for 23 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600

Protocol:
 Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 AmpliTaq Gold Polymerase: 0.07 units/ul
 Total Vol: 5 ul

Buffer:
 MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3

BAC end sequences from L. Hood at University of Washington.
 Designed and developed at the Stanford Human Genome Center.

FEATURES
 source
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 /organism="Homo sapiens"
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 primer_bind 82..286
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 BASE COUNT 113 a 131 c 112 g 121 t
 ORIGIN

Query Match 88.0%; Score 13.2; DB 54; Length 477;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGRCCTCCA 15
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 Db 142 GCTCCAGGACTCCA 156

RESULT 14
MMRARB3
LOCUS MMRARB3 534 bp mRNA ROD
DEFINITION Mouse RAR-beta mRNA for retinoic acid receptor-beta 3 isoform.
ACCESSION X56574
VERSION X56574.1 GI:53905
KEYWORDS RAR-beta gene; retinoic acid receptor; retinoic acid receptor beta
 2 isoform.
SOURCE house mouse.
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 534)
TITLE Chambon,P.
JOURNAL Direct Submission
 Submitted (08-NOV-1990) Chambon P., LGME/CRNS- U184/INSERM -
 Institute de Chimie Biologique, 11 rue Humann, 67085
 STRASBOURG-Cedex, France

REFERENCE
AUTHORS 2 (bases 1 to 534)
 Zelent,A., Mendelsohn,C., Kastner,P., Krust,A., Garnier,J.M.,
 Ruffenach,F., Leroy,P. and Chambon,P.
TITLE Differentially expressed isoforms of the mouse retinoic acid
 receptor beta generated by usage of two promoters and alternative
 splicing
JOURNAL EMBO J. 10 (1), 71-81 (1991)
MEDLINE 91114714
COMMENT See also X56569, X56573, X56574 for Murine RAR-beta isoforms. Data
 kindly reviewed (18-FEB-1991) by Chambon P.
FEATURES
 source
 1..534
 /organism="Mus musculus"
 /db_xref="taxon:10090"

Db 121 ACTCCATGGACTCCA 107
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RESULT 9
I49083/c
LOCUS I49083 396 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5627264.
ACCESSION I49083
VERSION I49083.1 GI:2467546
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 396)
AUTHORS Fodor, W.L., Rollins, S. and Squinto, S.P.
TITLE Chimeric complement inhibitor proteins
JOURNAL Patent: US 5627264-A 6 06-MAY-1997;
FEATURES
source 1..396
/organism="unknown"
BASE COUNT 98 a 96 c 95 g 107 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 10; Length 396;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RCTCCANGGRCTCCA 15
:||||| ||:|||||
Db 121 ACTCCATGGACTCCA 107

RESULT 10
SAICD59A/c
LOCUS SAICD59A 396 bp mRNA PRI 14-MAR-1994
DEFINITION Salmiri sciureus complement regulatory protein (CD59) mRNA,
complete cds.
ACCESSION L22859
VERSION L22859.1 GI:404796
KEYWORDS complement regulatory protein.
SOURCE Salmiri sciureus.
ORGANISM Salmiri sciureus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae;
Salmiri.
REFERENCE 1 (bases 1 to 396)
AUTHORS Rother, R.P., Rollins, S.A., Fodor, W.L., Albrecht, J.C., Setter, E.,
Fleckenstein, B. and Squinto, S.P.
TITLE Inhibition of complement-mediated cytolysis by the terminal
complement inhibitor of herpesvirus saimiri
J. Virol. 68 (2), 730-737 (1994)
JOURNAL 94118421
MEDLINE
FEATURES
source 1..396
/organism="Salmiri sciureus"
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gene
CDS

BASE COUNT 98 a 96 c 95 g 107 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 97; Length 396;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RCTCCANGGRCTCCA 15
:||||| ||:|||||
Db 121 ACTCCATGGACTCCA 107

RESULT 11
AF221064
LOCUS AF221064 413 bp mRNA ROD 07-MAR-2000
DEFINITION Meriones unguiculatus calcium-sensing receptor (CaSR) mRNA, partial
cds.
ACCESSION AF221064
VERSION AF221064.1 GI:7188643
KEYWORDS
SOURCE Mongolian gerbil.
ORGANISM Meriones unguiculatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
Meriones.
REFERENCE 1 (bases 1 to 413)
AUTHORS Wonneberger, K., Scofield, M.A. and Wangemann, P.
TITLE Evidence for a calcium sensing receptor in the vascular smooth
muscle cells of the spiral modiolar artery
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 413)
AUTHORS Wangemann, P. and Scofield, M.A.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2000) Pharmacology, Creighton University, 2500
California Plaza, Omaha, NE 68178, USA
FEATURES
source 1..413
/organism="Meriones unguiculatus"
/db_xref="taxon:10047"
/tissue_type="spiral modiolar artery; kidney"
1..413
/gene="CaSR"
1..413
/gene="CaSR"
/codon_start=3
/product="calcium-sensing receptor"
/protein_id="AAF37826.1"
/db_xref="GI:7188644"
/translation="AFKSRKLPENENAKFITFSLIFFIVWISFIPAYASTYGFVVS
AVEVITAAASFGLLACIFPNKYVYIILFKPSRNTIEVRCSSTAHAFAKVAARATLRRS
NVSRKSSSLGGSTGSIPISSSMSSKNSDEPPQP"

BASE COUNT 79 a 149 c 103 g 82 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 94; Length 413;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RCTCCANGGRCTCCA 15
:||||| ||:|||||
Db 343 GCTCCACGGGCTCCA 357

RESULT 12
AF018838/c
LOCUS AF018838 450 bp DNA INV 05-MAR-2001
DEFINITION Echinosmetra mathaei isolate Nm4 cytochrome oxidase subunit I gene,
partial cds; mitochondrial gene for mitochondrial product.
ACCESSION AF018838
VERSION AF018838.1 GI:2353671
KEYWORDS

exon
 HGPPSPGCGTSPATETQTSSEELVPS"
 317. .>360
 /gene="RAR-beta"
 /note="exon 4"
 BASE COUNT 74 a 125 c 80 g 81 t
 ORIGIN
 Query Match 88.0%; Score 13.2; DB 94; Length 360;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RCTCCANGGRCTCCA 15
 :||||| ||:|||||
 Db 258 ACTCCATGGGCTCCA 272
 RESULT 7
 LOCUS AR064381 396 bp DNA PAT 29-SEP-1999
 DEFINITION Sequence 3 from patent US 5847082.
 ACCESSION AR064381
 VERSION AR064381.1 GI:5993689
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 396)
 AUTHORS Rother,R., Rollins,S. and Squinto,S.P.
 TITLE Terminal complement inhibitor fusion proteins
 JOURNAL Patent: US 5847082-A 3 08-DEC-1998;
 FEATURES
 Location/Qualifiers
 source 1. .396
 /organism="unknown"
 BASE COUNT 98 a 96 c 95 g 107 t
 ORIGIN
 Query Match 88.0%; Score 13.2; DB 9; Length 396;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RCTCCANGGRCTCCA 15
 :||||| ||:|||||
 Db 121 ACTCCATGGACTCCA 107
 RESULT 8
 LOCUS I41335/c
 DEFINITION I41335 396 bp DNA PAT 13-MAY-1997
 ACCESSION Sequence 6 from patent US 5624837.
 VERSION I41335.1 GI:2081925
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 396)
 AUTHORS Fodor,W.L., Rollins,S. and Squinto,S.P.
 TITLE Nucleic acid encoding chimeric complement inhibitor proteins
 JOURNAL Patent: US 5624837-A 6 29-APR-1997;
 FEATURES
 Location/Qualifiers
 source 1. .396
 /organism="unknown"
 BASE COUNT 98 a 96 c 95 g 107 t
 ORIGIN
 Query Match 88.0%; Score 13.2; DB 10; Length 396;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RCTCCANGGRCTCCA 15

9 Cambridge Center, Cambridge MA 02142 USA

Tel: 617 252 1900

Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu

Primer A: AAACAAAAACAGCGCATGA

Primer B: CTTTGACCCACCTTGAGAGA

STS size: 277

PCR Profile:

Pesoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 nM

Tag Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from 238906 -- dbEST.

FEATURES

source Location/Qualifiers

STS 1..310 /organism="Homo sapiens"

primer_bind 33..309

primer_bind 33..52

BASE COUNT 89 a 90 c 50 g 81 t

ORIGIN

Query Match 88.0%; Score 13.2; DB 54; Length 310;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGCTCCA 15

Db 211 ACTCCAGGGGCTCCA 225

RESULT

E11372/c

ID E11372 standard; RNA; ROD; 324 BP.

XX AC E11372;

XX SV E11372.1

XX DT 07-OCT-1997 (Rel. 52, Created)

XX DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)

XX DE cDNA encoding mouse ligand-binding region protein(BC) of G-CSF receptor.

XX KW JP 1996131172-A/3.

XX OS Mus sp.

XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

XX RN [1]

XX RP 1-324

XX RA Ota Y., Anaguchi H.;

XX RT "DNA CODING PROTEIN BC IN LIGAND-BOUND REGION IN GRANULOCYTE COLONY

XX RT STIMULATING FACTOR RECEPTOR";

XX RL Patent number JP1996131172-A/3, 28-MAY-1996.

RL TANPAKU KOGAKU KENKYUSHO:KK.
XX OS Mus sp. (mouse)
CC PN JP 1996131172-A/3
CC PD 28-MAY-1996
CC PF 14-NOV-1994 JP 1994278841
CC PI Ota YOSHIMI, ANAGUCHI HIROYUKI
CC PC C12N15/09, C07H21/04, C07K14/715, C12N1/21, C12P21/02, (C12N1/21,
C12R1:19),
CC PC (C12P21/02, C12R1:19);
CC CC strandedness: Double;
CC CC topology: Linear;
CC CC hypothetical: No;
CC CC anti-sense: No; Location/Qualifiers
CC FH Key
CC FH source 1..324
CC FT /organism="Mus sp."
CC FT /clone="pMALp-mBC"
CC FT mat_peptide 1..324
CC FT /product="mouse ligand-binding region
CC FT protein(BC) of G-CSF
CC FT receptor"
XX FH Key Location/Qualifiers
FH FT source 1..324
FH FT /db_xref="taxon:10095"
FH FT /organism="Mus sp."
XX SQ Sequence 324 BP; 63 A; 103 C; 89 G; 69 T; 0 other;

Query Match 88.0%; Score 13.2; DB 45; Length 324;

Best Local Similarity 80.0%; Pred. No. 1.8e+03;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGCTCCA 15

Db 294 GCTCCAGGGGCTCCA 280

RESULT

DM128B5S

LOCUS 325 bp DNA STS 16-APR-1996

DEFINITION D. melanogaster STS determined from European Mapping Project

cosmid, sequence tagged site.

ACCESSION 271056

VERSION 271056.1 GI:1263558

KEYWORDS STS.

SOURCE fruit fly.

ORGANISM

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 325)

European Drosophila Mapping Consortium.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (15-APR-1996) Michael Ashburner, Department of Genetics,

Downing St., Cambridge CB2 3EH, England

STS_name = Dml28B5S

clone_name = 128B5

STS_from_promoter = SP6

vector_class = cosmid, Lorist 6

origin_of_clone = Oregon-R

in_situ_site.primary = 54F

BLAST_program = BLASTN

database_searched = EMBL

database_version = 45.0 and updates till date_of_search

date_of_search = 08-01-1996

BLAST_program = BLASTX

database_searched = SWISSPROT

database_version = 32.0


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c 9 13.2 88.0 396 10 I49083 Sequence 6
c 10 13.2 88.0 396 97 SAICDS59A
c 11 13.2 88.0 413 94 AF221064 Meriones
c 12 13.2 88.0 450 5 AF018838 Echinoset
c 13 13.2 88.0 477 54 G36845
c 14 13.2 88.0 534 94 MMRARB3
c 15 13.2 88.0 573 94 MMU276872
c 16 13.2 88.0 600 94 MMU276515
c 17 13.2 88.0 639 45 E09856
c 18 13.2 88.0 639 45 E11370
c 19 13.2 88.0 678 13 AF305546
c 20 13.2 88.0 700 72 AC057116
c 21 13.2 88.0 765 45 E11423
c 22 13.2 88.0 779 3 MxAORFAA
c 23 13.2 88.0 783 10 AX090395
c 24 13.2 88.0 783 94 MMU276870
c 25 13.2 88.0 792 10 AX068319
c 26 13.2 88.0 795 10 AX090391
c 27 13.2 88.0 802 95 S70577
c 28 13.2 88.0 810 94 MMU276514
c 29 13.2 88.0 819 91 CJU52115
c 30 13.2 88.0 834 10 AX090389
c 31 13.2 88.0 882 94 MMU276871
c 32 13.2 88.0 909 94 MMU276516
c 33 13.2 88.0 988 7 BTMP1
c 34 13.2 88.0 1001 53 CNS061Z1
c 35 13.2 88.0 1002 45 E11419
c 36 13.2 88.0 1051 53 CNS07740
c 37 13.2 88.0 1053 53 CNS060T1
c 38 13.2 88.0 1091 53 CNS062Y7
c 39 13.2 88.0 1107 2 AF334165
c 40 13.2 88.0 1110 88 AF073921
c 41 13.2 88.0 1114 93 HSM801875
c 42 13.2 88.0 1170 12 AB031003
c 43 13.2 88.0 1171 2 AY007557
c 44 13.2 88.0 1179 9 A27209
c 45 13.2 88.0 1179 58 AHSVVP7
```

ALIGNMENTS

```
RESULT 1
AX090397 LOCUS AX090397 26 bp DNA PAT 21-MAR-2001
DEFINITION Sequence 10 from Patent WO0116169.
ACCESSION AX090397
VERSION AX090397.1 GI:13444254
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM Ret ligand 5 (ret15) from human and mouse
REFERENCE 1 (bases 1 to 26)
AUTHORS Worley,D.
TITLE Ret ligand 5 (ret15) from human and mouse
JOURNAL Patent: WO 0116169-A 10 08-MAR-2001;
BIOMEDICAL, INC. (US)
FEATURES Location/Qualifiers
source
1..26
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"
BASE COUNT 6 a 8 c 10 g 2 t
ORIGIN
Query Match 88.0%; Score 13.2; DB 10; Length 26;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGCTCCA 15
:||||| ||:|||||
Db 4 GCTCCAGGGGCTCCA 18
```

```
RESULT 2
AB00468S29 LOCUS AB00468S29 84 bp DNA PRI 14-APR-2000
DEFINITION Human gene for Type XIX collagen al chain, exon 29.
ACCESSION AB004603
VERSION AB004603.1 GI:2598694
KEYWORDS Type XIX collagen al chain.
SEGMENT 29 of 52
SOURCE Homo sapiens DNA, clone:MKG34.
ORGANISM Homo sapiens
REFERENCE Eukaryotes; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Khaleduzzaman, H., Sumiyoshi, H., Ueki, Y., Inoguchi, K., Ninomiya, Y.
and Yoshioka, H.
TITLE Structure of the human type XIX collagen (COL19A1) gene, which
JOURNAL suggests it has arisen from an ancestor gene of the FACIT family
MEDLINE Genomics 45 (29), 304-312 (1997)
REFERENCE 98008918
AUTHORS Yoshioka, H.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-1997) to the DDBJ/EMBL/GenBank databases.
Hideoatsu Yoshioka, Okayama University Medical School, Molecular
Biology and Biochemistry; 2-5-1 Shikata-cho, Okayama, Okayama 700,
Japan (E-mail:mbb@ccw.ou.ac.jp, Tel:086-235-7128,
Fax:086-222-7768)
FEATURES Location/Qualifiers
source
1..84
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MKG34"
exon 16..69
/genes="COL19A1"
/number=29
BASE COUNT 14 a 24 c 22 g 24 t
ORIGIN
Query Match 88.0%; Score 13.2; DB 85; Length 84;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGCTCCA 15
:||||| ||:|||||
Db 46 ACTCCAGGGACTCCA 60

RESULT 3
G06299 LOCUS G06299 310 bp DNA STS 19-OCT-1995
DEFINITION human STS WI-6896.
ACCESSION G06299
VERSION G06299.1 GI:859544
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human STSs derived from sequences in dbEST and the Unigene
collection.
ORGANISM Homo sapiens
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
TITLE Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
JOURNAL Catarrhini; Hominidae; Homo.
COMMENT 1 (bases 1 to 310)
Hudson, T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
Unpublished (1995)
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
```

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:52:00 ; Search time 1774.1 Seconds
(without alignments)
130.780 Million cell updates/sec

Title: US-09-532-263-9
Perfect score: 15
Sequence: 1 RCTCCANGGRTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
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25: em_htg_hum4:*
26: em_htg_hum5:*
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33: em_htg_rod:*
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41: em_in:*
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43: em_or:*

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59: gb_vil2:*
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82: gb_htg23:*
83: gb_htg24:*
84: gb_htg25:*
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88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	13.2	88.0	26	10	AX090397	AX090397 Sequence
2	13.2	88.0	84	85	AB004603	AB004603 Human gen
3	13.2	88.0	310	54	G06299	G06299 human STS W
C 4	13.2	88.0	324	45	E11372	E11372 cDNA encodi
5	13.2	88.0	325	54	DM128855	Z71056 D. melanoga
6	13.2	88.0	360	94	MMRARB1	X36569 Mouse RAR-b
C 7	13.2	88.0	396	9	AR064381	AR064381 Sequence
C 8	13.2	88.0	396	10	I41335	I41335 Sequence 6

QY 1 RCTCCANGGRTCTCA 15
:||||| ||:|||||
Db 184 ACTCCAAGGACTCCA 170

RESULT 14
AAA67196
ID AAA67196 standard; DNA; 298 BP.
XX
AC AAA67196;
XX
DT 31-OCT-2000 (first entry)
XX
DE Eucalyptus grandis alpha-glucosidase DNA sequence SEQ ID NO:197.
XX
XX Eucalyptus grandis; pinus radiata; Monterey pine; modification;
KW plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
KW transgenic plant; ds.
XX
OS Eucalyptus grandis.
XX
PN WO200022092-A2.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-NZ00169.
XX
PR 13-OCT-1998; 98US-0170862.
PR 11-AUG-1999; 99US-0148426.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Bloksberg LN;
XX
DR WPI; 2000-339328/29.
XX
PT New genes encoding proteins involved in a plant polysaccharide
PT biosynthetic pathway, useful for modulating or altering the
PT polysaccharide content, composition or structure of the plant -

Claim 1; Page 126; 301pp; English.
XX The present invention describes isolated polynucleotides (PN) comprising
CC a sequence selected from one of 835 nucleotide sequences given in
CC AAA67073 to AAA67907, their (reverse) complements, sequences producing
CC an Expectation (E) value of 0.01 or less compared to the 835 sequences,
CC sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the
CC 835 sequences or sequences that are degenerately equivalent or allelic
CC to the 835 sequences. The polynucleotides are used to modify the
CC activity of a polypeptide involved in a polysaccharide biosynthetic
CC pathway in the plant. They are especially used to modulate or alter the
CC polysaccharide content, composition or structure of the plant. AAB16268
CC to AAB16340 are proteins encoded by some of the polynucleotide sequence
CC given in the present invention.
XX
SQ Sequence 298 BP; 77 A; 68 C; 75 G; 75 T; 3 other;

Query Match 88.0%; Score 13.2; DB 21; Length 298;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGRTCTCA 15
:||||| ||:|||||
Db 101 actccaagggtctcca 115

RESULT 15
AAA00475/c
ID AAA00475 standard; cDNA; 300 BP.
XX
AC AAA00475;

XX 19-MAY-2000 (first entry)
XX Human colon cancer cell line polynucleotide sequence SEQ ID NO:466.
DE
XX
XX Human; colon cancer; tumour; diagnosis; gene expression product;
KW probe; detection; cancerous state; metastasis; identification;
KW breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9958675-A2.
XX
PD 18-NOV-1999.
XX
PF 13-MAY-1999; 99WO-US10602.
XX
PR 14-MAY-1998; 98US-0085426.
PR 15-MAY-1998; 98US-0085537.
PR 15-MAY-1998; 98US-0085696.
PR 21-OCT-1998; 98US-0105234.
PR 27-OCT-1998; 98US-0105877.
XX
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
DR WPI; 2000-126369/11.
XX
XX Polynucleotide library used to determine cancerous states of mammalian
PT cells -

Claim 1; Page 291; 1097pp; English.
XX
XX AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
CC libraries constructed from human colon cancer cell lines. The present
CC invention also describes a method of detecting differentially expressed
CC genes correlated with a cancerous state of a mammalian cell, comprising
CC detecting at least one differentially expressed gene product in a test
CC sample derived from a cell suspected of being cancerous, where detection
CC of the differentially expressed gene product is correlated with a
CC cancerous state of the cell from which the test sample was derived.
CC The polynucleotides sequences can be used in a method for detecting
CC differentially expressed genes correlated with a cancerous state of a
CC mammalian cell. The polynucleotides can also be used as probes for
CC detecting and mapping related genes. They can be used in diagnosis and
CC prognosis of diseases and disorders (e.g. identification of
CC pre-metastatic or metastatic cancerous states, stages of cancer, or
CC responsiveness of cancer to therapy). This is particularly for breast
CC cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
CC negative breast cancer, lung cancer, and colon cancer.
XX
SQ Sequence 300 BP; 108 A; 38 C; 55 G; 99 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 300;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGRTCTCA 15
:||||| ||:|||||
Db 248 ACTCCACGGGCTCCA 234

Search completed: August 29, 2001, 20:16:43
Job time: 7424 sec

CC acute renal failure, acute nephritis, chronic renal failure, nephrotic
 CC syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic
 CC injury and trauma. The compounds are also useful for treating conditions
 CC such as neural degeneration where neural growth and regeneration are
 CC desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as
 CC motor neuron disease, demyelinating disease, bacterial diseases, viral
 CC diseases, and prion diseases including Creutzfeldt-Jakob disease. The
 CC compounds are also useful for treating disorders due to damage to neural
 CC tissue caused by neoplastic impingement, trauma or cerebrovascular events
 CC such as hemorrhage or emboli, and neural disorders such as mental
 CC retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral
 CC palsy. The present sequence represents an antisense oligo KD2-619 used in
 CC the characterisation of genomic clones for RetL5.
 XX
 SQ Sequence 26 BP; 6 A; 8 C; 10 G; 2 T; 0 other;

Query Match 88.0%; Score 13.2; DB 22; Length 26;
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGRCTCCA 15
 :||||| ||:|||||
 Db 4 gctccagggggtcca 18

RESULT 12
 AAV55971/c
 ID AAV55971 standard; DNA; 204 BP.

AC AAV55971;

XX 18-JAN-1999 (first entry)

DE Human cytokine receptor Zcytor4 expressed sequence tag.

XX Cytokine receptor; Zcytor4; human; cell proliferation;
 KW cell differentiation; cell adhesion; Burkitt's lymphoma;
 KW leukaemia; diagnosis; ss.

XX Homo sapiens.

XX WO9842836-A1.

XX 01-OCT-1998.

XX 18-MAR-1998; 98WO-US05254.

XX 21-MAR-1997; 97US-0041570.

XX (ZYMO) ZYMOGENETICS INC.

PI Adams RL, Farrah TM, Kho CJ, Lok S, Pownder TA;
 PI Whitmore T;

XX WPI; 1998-542279/46.

XX Human and mouse cytokine receptors, DNA and antibodies - also
 PT chimeric proteins, useful for promoting cell adhesion and diagnosing
 PT Burkitt's lymphoma and leukaemia

XX Example 1; Page 52; 66pp; English.

XX This is the nucleotide sequence of an expressed sequence tag
 CC identified during the cloning of human cytokine receptor Zcytor4
 CC cDNA (see AAV55968). A cDNA containing 2130 bp was obtained from a
 CC human kidney cDNA library. The DNA was transfected into
 CC Escherichia coli strain DH10b and the plasmid was designated
 CC pSL6907. This has been used to generate probes to examine
 CC expression of Zcytor4. The invention provides Zcytor4
 CC polynucleotides (see AAV55968) and polypeptides (see AAW80754-56),
 CC expression vectors, eukaryotic host cells which express Zcytor4

CC polypeptide, chimeric proteins comprising Zcytor4 polypeptide and
 CC an affinity tag, and antibodies that specifically bind Zcytor4.
 CC Zcytor4 may play a role in intracellular adhesion and in the
 CC regulation or development of haematopoietic cells.

SQ Sequence 204 BP; 45 A; 45 C; 55 G; 51 T; 8 other;

Query Match 88.0%; Score 13.2; DB 19; Length 204;
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGRCTCCA 15
 :||||| ||:|||||
 Db 57 ACTCCAAGGACTCCA 43

RESULT 13
 AAV55980/c
 ID AAV55980 standard; DNA; 211 BP.

XX AC AAV55980;

XX 18-JAN-1999 (first entry)

DE Human cytokine receptor Zcytor4 DNA probe.

XX Cytokine receptor; Zcytor4; human; cell proliferation;
 KW cell differentiation; cell adhesion; Burkitt's lymphoma;
 KW leukaemia; diagnosis; probe; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9842836-A1.

XX 01-OCT-1998.

XX 18-MAR-1998; 98WO-US05254.

XX 21-MAR-1997; 97US-0041570.

XX (ZYMO) ZYMOGENETICS INC.

XX Adams RL, Farrah TM, Kho CJ, Lok S, Pownder TA;
 PI Whitmore T;

XX WPI; 1998-542279/46.

XX Human and mouse cytokine receptors, DNA and antibodies - also
 PT chimeric proteins, useful for promoting cell adhesion and diagnosing
 PT Burkitt's lymphoma and leukaemia

XX Example 1; Page 55; 66pp; English.

XX This polynucleotide was generated as a probe for the isolation of
 CC novel human cytokine receptor Zcytor4 cDNA. It was generated by
 CC PCR amplification (see AAV55972 and AAV55972) of a human foetal kidney
 CC cDNA library. The invention provides human and mouse cytokine
 CC receptor Zcytor4 polynucleotides (see AAV55968-69) and polypeptides
 CC (see AAW80754-57), expression vectors, eukaryotic host cells which
 CC express Zcytor4, chimeric proteins comprising a Zcytor4 polypeptide
 CC and an affinity tag, and antibodies that specifically bind Zcytor4.
 CC Zcytor4 may play a role in intracellular adhesion and in the
 CC regulation or development of haematopoietic cells.

SQ Sequence 211 BP; 57 A; 45 C; 51 G; 58 T; 0 other;

Query Match 88.0%; Score 13.2; DB 19; Length 211;
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

PD 29-DEC-1999.
 XX
 PF 23-JUN-1999; 99WO-JP03351.
 XX
 PR 24-JUN-1998; 98JP-0214720.
 PR 19-OCT-1998; 98JP-0297409.
 XX
 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 XX Nomura H, Maeda M;
 PI WPI; 2000-116933/10.
 DR
 XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders -
 PT
 XX Example 1; Page 43; 176pp; Japanese.
 PS
 XX The invention relates to the isolation of sequences encoding human
 CC haemopoietin receptor protein family NR8 genes. The NR8 family
 CC sequences were initially searched for comparison on a nucleic acid
 CC database with the nucleic acid probe sequence TCGAGYNNNTGGAGY encoding
 CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 CC AA259258-259300 and AA290816-290925 represent specific examples of probe
 CC sequences used in the search. Antibodies to the NR8 family proteins are
 CC used for the diagnosis of blood formation disorders. Compounds identified
 CC as binding to the proteins are used for the treatment of such disorders.
 XX
 SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGRTCCCA 15
 :||||| ||:|||||
 Db 15 GCTCCAAGGGCTCCA 1

RESULT 10
 AAZ90922/c
 ID AAZ90922 standard; DNA; 15 BP.
 XX
 AC AAZ90922;

DT 24-MAY-2000 (first entry)

DE Human NR8 gene probe #150.

KW Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder; fusion protein; probe; ss.

OS Homo sapiens.

PN WO9967290-A1.

XX 29-DEC-1999.

PF 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

PR 19-OCT-1998; 98JP-0297409.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders -
 PT

PS Example 1; Page 45; 176pp; Japanese.
 XX
 CC The invention relates to the isolation of sequences encoding human
 CC haemopoietin receptor protein family NR8 genes. The NR8 family
 CC sequences were initially searched for comparison on a nucleic acid
 CC database with the nucleic acid probe sequence TCGAGYNNNTGGAGY encoding
 CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 CC AA259258-259300 and AA290816-290925 represent specific examples of probe
 CC sequences used in the search. Antibodies to the NR8 family proteins are
 CC used for the diagnosis of blood formation disorders. Compounds identified
 CC as binding to the proteins are used for the treatment of such disorders.
 XX
 SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGRTCCCA 15
 :||||| ||:|||||
 Db 15 GCTCCAAGGGCTCCA 1

RESULT 11
 AAF57274
 ID AAF57274 standard; DNA; 26 BP.
 XX
 AC AAF57274;

XX 29-MAY-2001 (first entry)

DE Antisense oligo KD2-819 for RetL5 genomic clones characterisation.

KW Ret ligand 5; RetL5; autophosphorylation; tumour; renal; nephrotropic;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; mouse;
 KW vulnary; nootropic; anti-HIV; neuroprotective; antibacterial; ss;
 KW cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic.

OS Mus sp.

PN WO200116169-A2.

XX 08-MAR-2001.

PF 01-SEP-2000; 2000WO-US24111.

PR 01-SEP-1999; 99US-0152024.

XX (BIOJ) BIOGEN INC.

XX Worley D;

XX WPI; 2001-235091/24.

XX Novel Ret ligand polypeptide useful for suppressing growth of a tumor
 PT cell that expresses Ret and for modulating Ret signal transduction
 PT involving a cell expressing Ret polypeptide or Ret ligand polypeptide
 PT

PS Example 5; Page 33; 76pp; English.

XX The invention relates to mouse and human Ret ligand 5 (RetL5)
 CC polypeptides. The RetL5 polypeptides can be expressed by standard
 CC recombinant methodology. The RetL5 when bound to Ret, acts as a
 CC dimerization or autophosphorylation activator. The polypeptides and their
 CC antibodies are useful for stimulating growth of or limiting damage to,
 CC Ret expressing tissue in a subject, for suppressing growth of a tumour
 CC cell that expresses Ret, for modulating Ret signal transduction involving
 CC a cell expressing the Ret polypeptide. The RetL5 polypeptides, fusion
 CC proteins containing RetL5 and antibodies are useful for stimulating renal
 CC tissue growth and/or survival, supporting renal function and minimizing
 CC damage to renal tissue after various insults, particularly for treating

CC used for the diagnosis of blood formation disorders. Compounds identified
 CC as binding to the proteins are used for the treatment of such disorders.

SQ Sequence 15 BP; 2 A; 3 C; 6 G; 4 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGRCCTCCA 15
 :||||| ||:|||||
 Db 15 GCTCCAAGGACTCCA 1

RESULT 7

AAZ90863/c
 ID AAZ90863 standard; DNA; 15 BP.

AC AAZ90863;

XX 24-MAY-2000 (first entry)

XX Human NR8 gene probe #91.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder; fusion protein; probe; ss.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 formation disorders -
 Example 1; Page 42; 176pp; Japanese.

The invention relates to the isolation of sequences encoding human
 haemopoietin receptor protein family NR8 genes. The NR8 family
 sequences were initially searched for comparison on a nucleic acid
 database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
 the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
 sequences used in the search. Antibodies to the NR8 family proteins are
 used for the diagnosis of blood formation disorders. Compounds identified
 as binding to the proteins are used for the treatment of such disorders.

SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGRCCTCCA 15
 :||||| ||:|||||
 Db 15 ACTCCAGGGCTCCA 1

RESULT 8

AAZ90885/c

ID AAZ90885 standard; DNA; 15 BP.

AC AAZ90885;

XX 24-MAY-2000 (first entry)

XX Human NR8 gene probe #118.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder; fusion protein; probe; ss.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 formation disorders -
 Example 1; Page 43; 176pp; Japanese.

The invention relates to the isolation of sequences encoding human
 haemopoietin receptor protein family NR8 genes. The NR8 family
 sequences were initially searched for comparison on a nucleic acid
 database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
 the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
 sequences used in the search. Antibodies to the NR8 family proteins are
 used for the diagnosis of blood formation disorders. Compounds identified
 as binding to the proteins are used for the treatment of such disorders.

SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGRCCTCCA 15
 :||||| ||:|||||
 Db 15 GCTCCAAGGACTCCA 1

AAZ90885/c
 ID AAZ90885 standard; DNA; 15 BP.

XX AAZ90885;

XX 24-MAY-2000 (first entry)

XX Human NR8 gene probe #113.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder; fusion protein; probe; ss.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 formation disorders -
 Example 1; Page 43; 176pp; Japanese.

The invention relates to the isolation of sequences encoding human
 haemopoietin receptor protein family NR8 genes. The NR8 family
 sequences were initially searched for comparison on a nucleic acid
 database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
 the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 AAZ59258-Z59300 and AAZ90816-Z90925 represent specific examples of probe
 sequences used in the search. Antibodies to the NR8 family proteins are
 used for the diagnosis of blood formation disorders. Compounds identified
 as binding to the proteins are used for the treatment of such disorders.

SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGRCCTCCA 15
 :||||| ||:|||||
 Db 15 GCTCCAAGGACTCCA 1

RESULT 9

AAZ90890/c

ID AAZ90890 standard; DNA; 15 BP.

AC AAZ90890;

XX 24-MAY-2000 (first entry)

XX Human NR8 gene probe #118.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder; fusion protein; probe; ss.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
OS Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood

XX formation disorders -

XX Example 1; Page 40; 176pp; Japanese.

XX The invention relates to the isolation of sequences encoding human

XX haemopoietin receptor protein family NR8 genes. The NR8 family

XX sequences were initially searched for comparison on a nucleic acid

XX database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding

XX the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences

XX AA259258-259300 and AA290816-290925 represent specific examples of probe

XX sequences used in the search. Antibodies to the NR8 family proteins are

XX used for the diagnosis of blood formation disorders. Compounds identified

XX as binding to the proteins are used for the treatment of such disorders.

XX Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;

XX Query Match 88.0%; Score 13.2; DB 21; Length 15;

XX Best Local Similarity 80.0%; Pred. No. 5.1e+02;

XX Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

XX QY 1 RCTCCANGGRCCTCCA 15

XX :||||| ||:|||||

XX Db 15 GCTCCAGGGACTCCA 1

XX RESULT 5

XX AA290850/c

XX ID AA290850 standard; DNA; 15 BP.

XX AC AA290850;

XX 24-MAY-2000 (first entry)

XX Human NR8 gene probe #78.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;

XX blood formation disorder; fusion protein; probe; ss.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

PI Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood

XX formation disorders -

XX Example 1; Page 41; 176pp; Japanese.

XX The invention relates to the isolation of sequences encoding human

XX haemopoietin receptor protein family NR8 genes. The NR8 family

XX sequences were initially searched for comparison on a nucleic acid

XX database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding

XX the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences

XX AA259258-259300 and AA290816-290925 represent specific examples of probe

XX sequences used in the search. Antibodies to the NR8 family proteins are

XX used for the diagnosis of blood formation disorders. Compounds identified

XX as binding to the proteins are used for the treatment of such disorders.

XX Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;

XX Query Match 88.0%; Score 13.2; DB 21; Length 15;

XX Best Local Similarity 80.0%; Pred. No. 5.1e+02;

XX Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

XX QY 1 RCTCCANGGRCCTCCA 15

XX :||||| ||:|||||

XX Db 15 GCTCCAGGGACTCCA 1

XX RESULT 6

XX AA290853/c

XX ID AA290853 standard; DNA; 15 BP.

XX AC AA290853;

XX 24-MAY-2000 (first entry)

XX Human NR8 gene probe #81.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;

XX blood formation disorder; fusion protein; probe; ss.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood

XX formation disorders -

XX Example 1; Page 41; 176pp; Japanese.

XX The invention relates to the isolation of sequences encoding human

XX haemopoietin receptor protein family NR8 genes. The NR8 family

PS Claim 12; Page 52; 87pp; English.

CC 5 Degenerate hybridisation probes (AA17870-74) are based on a conserved motif (AAR92812) found in haemopoietin receptors. The CC probes are used in the identification and/or cloning of genes CC coding for novel haemopoietin receptors, e.g. the murine CC interleukin-11 (IL-11) receptor alpha chain gene (AA117868). Such CC receptors are defined by their ability to hybridise to the CC probes under medium stringency conditions.

XX

SQ Sequence 15 BP; 2 A; 6 C; 2 G; 2 T; 3 other;

Query Match 88.0%; Score 13.2; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCANGGRTCCA 15
Db ||||| |||||

RESULT 2
AAZ59273/C
ID AAZ59273 standard; DNA; 15 BP.
XX AC AAZ59273;
XX

DT 24-MAY-2000 (first entry)
XX

DE Human NR8 gene probe #61.
XX

KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX

OS Homo sapiens.
XX

PN WO9967290-A1.
XX

PD 29-DEC-1999.
XX

PF 23-JUN-1999; 99WO-JP03351.
XX

PR 24-JUN-1998; 98JP-0214720.
XX

PR 19-OCT-1998; 98JP-0297409.
XX

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX

PI Nomura H, Maeda M;
XX

DR WPI; 2000-116933/10.
XX

PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT formation disorders -
XX

PS Example 1; Page 40; 176pp; Japanese.
XX

CC The invention relates to the isolation of sequences encoding human
CC haemopoietin receptor protein family NR8 genes. The NR8 family
CC sequences were initially searched for comparison on a nucleic acid
CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
CC AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
CC sequences used in the search. Antibodies to the NR8 family proteins are
CC used for the diagnosis of blood formation disorders. Compounds identified
CC as binding to the proteins are used for the treatment of such disorders.
XX

SQ Sequence 15 BP; 2 A; 6 C; 2 G; 4 T; 0 other;

Query Match 88.0%; Score 13.2; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCANGGRTCCA 15
Db ||||| |||||

RESULT 4
AAZ90834/C
ID AAZ90834 standard; DNA; 15 BP.
XX AC AAZ90834;
XX

DT 24-MAY-2000 (first entry)
XX

DE Human NR8 gene probe #62.
XX

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 20:16:43 ; Search time 301.32 Seconds
(without alignments)
31.258 Million cell updates/sec

Title: US-09-532-263-9

Perfect score: 15

Sequence: 1 RCTCCAGGRCCTCCA 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0601.*

- 1: /SIDS8/gcgdata/geneseq/geneseqn/NA1980.DAT.*
- 2: /SIDS8/gcgdata/geneseq/geneseqn/NA1981.DAT.*
- 3: /SIDS8/gcgdata/geneseq/geneseqn/NA1982.DAT.*
- 4: /SIDS8/gcgdata/geneseq/geneseqn/NA1983.DAT.*
- 5: /SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT.*
- 6: /SIDS8/gcgdata/geneseq/geneseqn/NA1985.DAT.*
- 7: /SIDS8/gcgdata/geneseq/geneseqn/NA1986.DAT.*
- 8: /SIDS8/gcgdata/geneseq/geneseqn/NA1987.DAT.*
- 9: /SIDS8/gcgdata/geneseq/geneseqn/NA1988.DAT.*
- 10: /SIDS8/gcgdata/geneseq/geneseqn/NA1989.DAT.*
- 11: /SIDS8/gcgdata/geneseq/geneseqn/NA1990.DAT.*
- 12: /SIDS8/gcgdata/geneseq/geneseqn/NA1991.DAT.*
- 13: /SIDS8/gcgdata/geneseq/geneseqn/NA1992.DAT.*
- 14: /SIDS8/gcgdata/geneseq/geneseqn/NA1993.DAT.*
- 15: /SIDS8/gcgdata/geneseq/geneseqn/NA1994.DAT.*
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- 19: /SIDS8/gcgdata/geneseq/geneseqn/NA1998.DAT.*
- 20: /SIDS8/gcgdata/geneseq/geneseqn/NA1999.DAT.*
- 21: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT.*
- 22: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	13.2	88.0	15	17	AAT17873		Haemopoietin recep
2	13.2	88.0	15	21	AZ59273		Human NR8 gene pro
3	13.2	88.0	15	21	AZ90833		Human NR8 gene pro
4	13.2	88.0	15	21	AZ90834		Human NR8 gene pro
5	13.2	88.0	15	21	AZ90850		Human NR8 gene pro
6	13.2	88.0	15	21	AZ90853		Human NR8 gene pro
7	13.2	88.0	15	21	AZ90863		Human NR8 gene pro
8	13.2	88.0	15	21	AZ90865		Human NR8 gene pro
9	13.2	88.0	15	21	AZ90890		Human NR8 gene pro
10	13.2	88.0	15	21	AZ90922		Human NR8 gene pro
11	13.2	88.0	26	22	AAF57274		Antisense oligo KD

C 12	13.2	88.0	204	19	AAV55971	Human cytokine rec
C 13	13.2	88.0	211	19	AAV55980	Human cytokine rec
C 14	13.2	88.0	298	21	AA67196	Eucalyptus grandis
C 15	13.2	88.0	300	21	AAA00475	Human colon cancer
C 16	13.2	88.0	324	17	AAT33517	G-CSF receptor lig
C 17	13.2	88.0	349	21	AAZ42586	Human 5' EST isola
C 18	13.2	88.0	396	16	AAQ84638	Squirrel Monkey co
C 19	13.2	88.0	396	16	AAQ99109	SQMCP full-length
C 20	13.2	88.0	396	16	AAQ03334	Ly-6 terminal CIP
C 21	13.2	88.0	639	17	AAT33515	Mouse G-CSF recept
C 22	13.2	88.0	725	21	AAA02109	Human colon cancer
C 23	13.2	88.0	765	17	AAT35141	DNA encoding cytok
C 24	13.2	88.0	783	22	AAF57273	Mouse RetL5 altern
C 25	13.2	88.0	792	22	AAF31057	Murine EST AU03593
C 26	13.2	88.0	795	22	AAF57271	Mouse RetL5 polytype
C 27	13.2	88.0	795	22	AAC84378	Human TANGO 204 po
C 28	13.2	88.0	795	22	AAC84386	Mouse TANGO 204 po
C 29	13.2	88.0	834	22	AAF57270	Mouse RetL5 polytype
C 30	13.2	88.0	1002	17	AAT35137	DNA encoding cytok
C 31	13.2	88.0	1019	20	AAZ28259	Murine glial deriv
C 32	13.2	88.0	1178	13	AAQ30130	Gene for AHSV. Af
C 33	13.2	88.0	1293	22	AAC84385	Mouse TANGO 204 po
C 34	13.2	88.0	1293	22	AAC84396	Mouse TANGO 204 va
C 35	13.2	88.0	1293	22	AAC84397	Mouse TANGO 204 va
C 36	13.2	88.0	1293	22	AAC84398	Mouse TANGO 204 va
C 37	13.2	88.0	1590	19	AAV63614	DNA sequence encod
C 38	13.2	88.0	1590	19	AAV63541	DNA sequence encod
C 39	13.2	88.0	1607	21	AAF15587	Human prostate can
C 40	13.2	88.0	1656	19	AAV02978	Human interleukin-
C 41	13.2	88.0	1874	21	AAF21936	Human breast and o
C 42	13.2	88.0	1974	21	AAC77172	Human ORFX ORF2727
C 43	13.2	88.0	1998	20	AAZ00367	Nucleotide sequenc
C 44	13.2	88.0	2087	20	AAZ00343	Nucleotide sequenc
C 45	13.2	88.0	2166	20	AAZ00379	Nucleotide sequenc

ALIGNMENTS

RESULT 1	
AAT17873	
ID	AAT17873 standard; DNA; 15 BP.
XX	
AC	AAT17873;
XX	
DT	21-MAY-1996 (first entry)
XX	
DE	Haemopoietin receptor probe HYB4.
XX	
KW	Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
KW	therapy; diagnosis; probe; hybridisation; ss.
XX	
OS	Synthetic.
XX	
PN	WO9607737-A1.
XX	
PD	14-MAR-1996.
XX	
PF	05-SEP-1995; 95WO-AU00578.
XX	
PR	05-SEP-1994; 94AU-0007902.
PR	05-SEP-1994; 94AU-0007901.
XX	
PA	(AMRA-) AMRAD OPERATIONS PTY LTD.
XX	
PI	Hilton DJ;
XX	
DR	WPI; 1996-171612/17.
XX	

Nucleic acid encoding haemopoietin receptor containing conserved amino acid motif esp. IL-11 receptor alpha chain - used for developing IL-11 (ant)agonists

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGGCTCCA 15
:||||| ||:|||||
Db 66 GCTCCAGGGACTCCA 52

RESULT 15

D45552 235 bp mRNA EST 20-FEB-1995
LOCUS HUMGS02739 Human adult lung 3' directed MboI cDNA Homo sapiens cDNA
DEFINITION 3', mRNA sequence.

ACCESSION D45552

VERSION D45552.1 GI:662506

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 235)

AUTHORS Itoh,K., Okubo,K., Yosii,J., Yokouchi,H. and Matsubara,K.

TITLE An expression profile of active genes in human lung

JOURNAL DNA Research 1, 279-287 (1994)

MEDLINE 95236275

COMMENT

Contact: Kohichi Itoh

Institute for Molecular and Cellular Biology

Osaka University

3-1, Yamadaoka, Suita, Osaka, 565, Japan

Tel: 06-877-5111 x3910

Fax: 06-877-1922

FEATURES

source

1. .235

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Human adult lung 3' directed MboI cDNA"

/notes="Adult human lung, 3' directed MboI"

41 a 85 c 55 g 48 t 6 others

BASE COUNT

ORIGIN

Query Match 88.0%; Score 13.2; DB 156; Length 235;

Best Local Similarity 80.0%; Pred. No. 5.5e+03;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGGCTCCA 15

:||||| ||:|||||

Db 197 GCTCCAGGGACTCCA 211

Search completed: August 29, 2001, 19:22:17
Job time: 24140 sec

GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot - 10.0 and subtraction to Rot - 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAATTAATCCGCCGCCGCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pluescript KS(+) after bulk excision from Lambda FIC I. Cloning sites, 5' end: SalI; 3' end: BamHI.

BASE COUNT 47 a 49 c 53 g 53 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 29; Length 202;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGGCTCCCA 15
:||||| ||:|||||
DB 60 GCTCCAGGGCTCCCA 46

RESULT 9
LOCUS BF380015 221 bp mRNA EST 27-NOV-2000
DEFINITION MRO-UT0047-080900-201-007 UT0047 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF380015
VERSION BF380015.1 GI:11369140
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 221)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0st2-MR0-UT0047-080900-201-d07&t3=2000-09-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 56
High quality sequence stop: 219
Location/Qualifiers
1. 221

FEATURES
source
1. 221
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UT0047"
/dev_stage="Adult"
/note="Organ: uterus.tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under

BASE COUNT 69 a 45 c 57 g 50 t
ORIGIN

Query Match 88.0%; Score 13.2; DB 148; Length 221;
Best Local Similarity 80.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGGCTCCCA 15
:||||| ||:|||||
DB 200 GCTCCATGGACTCCA 214

RESULT 10
LOCUS AW462741/c 226 bp mRNA EST 24-FEB-2000
DEFINITION BP230010A20B6 Soares normalized bovine placenta cDNA clone BP230010A20B6 5', mRNA sequence.
ACCESSION AW462741
VERSION AW462741.1 GI:7032909
KEYWORDS EST.
SOURCE cow.

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 226)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson,J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmer q: Cross_match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTAACCTCACTAAAG
Insert Length: 226 Std Error: 0.00
Plate: BP230010A20 row: B column: 6
Seq primer: ACGGATACCAATTCACACAGGA
High quality sequence stop: 226.
Location/Qualifiers
1. 226

FEATURES
source

1. 226
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP230010A20B6"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was constructed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806."
52 a 49 c 60 g 65 t

BASE COUNT
ORIGIN

Query Match 88.0%; Score 13.2; DB 116; Length 226;
Best Local Similarity 80.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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mRNA and cDNA amplification were performed under low
stringency conditions."
55 a 46 c 49 g 48 t
BASE COUNT
ORIGIN

Query Match      88.0%; Score 13.2; DB 120; Length 198;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGGCTCCA 15
      ||||| ||:|||||
Db 67 ACTCCAGGACTCCA 81

RESULT 7
AA163051 199 bp mRNA EST 12-FEB-1997
LOCUS me24a10.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION IMAGE:607866 5', mRNA sequence.
ACCESSION AA163051
VERSION AA163051.1 GI:1739014
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:373298
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 183.
FEATURES
Source Location/Qualifiers
1..199
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:607866"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1: ECORI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 Kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCAGG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT 47 a 39 c 49 g 64 t
ORIGIN

Query Match      88.0%; Score 13.2; DB 3; Length 199;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCTCCANGGCTCCA 15
      ||||| ||:|||||
Db 67 ACTCCAGGACTCCA 81

RESULT 8
AV340647 202 bp mRNA EST 11-NOV-1999
LOCUS AV340647 RIKEN full-length enriched, adult male olfactory bulb Mus
DEFINITION musculus cDNA clone 6430516D09 3', mRNA sequence.
ACCESSION AV340647
VERSION AV340647.1 GI:6380699
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai
, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata
, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, T., Suzuki, H.,
Suzuki, H., Takahashi, F., Tateo, M., Tomimaga, N., Tsunoda, Y.,
Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,
Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp/
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki
, Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
Source Location/Qualifiers
1..202
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6430516D09"
/clone_lib="RIKEN full-length enriched, adult male
olfactory bulb"
/sex="male"
/tissue_type="olfactory brain"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'

```

Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigenoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.

TITLE JOURNAL COMMENT

RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa

Genome Science Laboratory

RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-reser@rctc.riken.go.jp

Thermotabilization and thermostabilization of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES source

Location/Qualifiers

1..187

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="2610207N04"

/clone_lib="Mus musculus C57BL/6J 10-day embryo"

/sex="mixed"

/dev_stage="10-day embryo"

58 a 40 c 37 g 47 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 13.2; DB 25; Length 182;

Best Local Similarity 80.0%; Pred. No. 5.4e+03;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGGRCCTCCA 15

Db :||||| :|||||

Db 42 ACTCCATGGACTCCA 56

RESULT

5

AI933508/C

LOCUS

DEFINITION wm74e06.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2441698 3',

mRNA sequence.

ACCESSION AI933508

VERSION AI933508.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 187)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

Tumor Gene Index

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

Cloning Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.lnlni.gov/bbrp/image/image.html

Insert Length: 1894 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 133.

FEATURES source

Location/Qualifiers

1..187

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2441698"

/clone_lib="NCI_CGAP_Ut2"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.85 kb. Life Technologies catalog #:

11539-012"

36 a 42 c 62 g 47 t

BASE COUNT

ORIGIN

Query Match 88.0%; Score 13.2; DB 103; Length 187;

Best Local Similarity 80.0%; Pred. No. 5.4e+03;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGGRCCTCCA 15

Db :||||| :|||||

Db 55 GCTCCAGGACTCCA 41

RESULT

6

AW804893

LOCUS

DEFINITION QV4-UM0094-280300-152-a01 UM0094 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW804893

VERSION AW804893.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 198)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-QV4-UM0094-280>)

300-152-a01&t3=2000-03-28&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 198.

Location/Qualifiers

1..198

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="UM0094"

/dev_stage="Adult"

/note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

, 716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbrrp/image/image.html
 Insert length: 632 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 107.

FEATURES

Source
 1..151
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2011202"
 /clone_lib="NCI_CGAP_Brn23"
 /tissue_type="glioblastoma (pooled)"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAAGTGGGAGCGGCATATCTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
 BASE COUNT 33 a 37 c 50 g 31 t
 ORIGIN

Query Match 88.0%; Score 13.2; DB 19; Length 151;
 Best Local Similarity 80.0%; Pred. NO. 5.3e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGGCTCCA 15
 Db 42 GCTCCAGGGACTCCA 28

RESULT 3
 LOCUS BB593914/c 170 bp mRNA EST 30-NOV-2000
 DEFINITION BB593914 RIKEN full-length enriched, 4 days neonate male adipose Mus musculus cDNA clone B430304H06 5', mRNA sequence.

ACCESSION BB593914
 VERSION BB593914.1 GI:11490516

KEYWORDS EST.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodojima,Y., Konno Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno ,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka ,T., Taya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
 Unpublished (2000)
 Contact: Yoshihide Hayashizaki
 Genome Exploration Research Group, Life Science Tsukuba Center,
 The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: +81-298-36-9013
 Fax: +81-298-36-9098
 Email: genome-res@rtrc.riken.go.jp,

TITLE JOURNAL COMMENT

URL:[http://genome.rtc.riken.go.jp](http://genome.rtc.riken.go.jp/Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki ,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (<a href=)) for further details.

FEATURES

Source
 1..170
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="B430304H06"
 /clone_lib="RIKEN full-length enriched, 4 days neonate male adipose"
 /sex="male"
 /tissue_type="adipose"
 /dev_stage="4 days neonate"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 229.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAAATTAATCCCTCCCTCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda F1C I."

BASE COUNT 34 a 54 c 50 g 32 t
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Query Match 88.0%; Score 13.2; DB 161; Length 170;
 Best Local Similarity 80.0%; Pred. NO. 5.4e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCTCCAGGCTCCA 15
 Db 58 GCTCCAGGGCTCCA 44

RESULT 4

LOCUS AV118281 182 bp mRNA EST 30-JUN-1999
 DEFINITION AV118281 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2610207N04, mRNA sequence.

ACCESSION AV118281
 VERSION AV118281.1 GI:5300432

KEYWORDS EST.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 182)
 Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	13.2	88.0	100	10	AA644792	AA644792 vs82d07.r	
C	2	13.2	88.0	151	19	AI371456	AI371456 qy06c02.x
	3	13.2	88.0	170	161	BB593914	BB593914 BB593914
C	4	13.2	88.0	182	25	AV118281	AV118281 AV118281
	5	13.2	88.0	187	103	AI933508	AI933508 wm74e06.x
C	6	13.2	88.0	198	120	AW804893	AW804893 QV4-UM009
	7	13.2	88.0	199	3	AA163051	AA163051 ms24a10.r
C	8	13.2	88.0	202	29	AV340647	AV340647 AV340647
	9	13.2	88.0	221	148	BF380015	BF380015 MR0-UT004
C	10	13.2	88.0	226	116	AW62741	AW62741 BP230010A
	11	13.2	88.0	227	28	AV282369	AV282369 AV282369
C	12	13.2	88.0	230	28	AV288298	AV288298 AV288298
	13	13.2	88.0	232	17	A1234857	A1234857 EST231419
C	14	13.2	88.0	233	9	AA587324	AA587324 nn78e01.s
	15	13.2	88.0	235	156	D45552	D45552 HUMG02739
C	16	13.2	88.0	236	2	AA089075	AA089075 mo63a01.r
	17	13.2	88.0	237	188	T03328	T03328 IB1253 Infa
C	18	13.2	88.0	240	156	C12571	C12571 C12571 Yuji
	19	13.2	88.0	246	158	H32365	H32365 EST107377.R
C	20	13.2	88.0	250	17	AI185438	AI185438 qe53d09.x
	21	13.2	88.0	250	127	BB180104	BB180104 BB180104
C	22	13.2	88.0	251	157	F37625	F37625 HSPD05393.H
	23	13.2	88.0	253	10	AA653297	AA653297 ag65c06.s
C	24	13.2	88.0	255	157	F01487	F01487 HSC04D122.n
	25	13.2	88.0	256	5	AA340930	AA340930 EST46241
C	26	13.2	88.0	260	168	BF714533	BF714533 mab01e01.
	27	13.2	88.0	262	131	BB313512	BB313512 BB313512
C	28	13.2	88.0	264	21	AI547450	AI547450 UI-R-C3-s
	29	13.2	88.0	268	8	AA494436	AA494436 ne28d04.s
C	30	13.2	88.0	271	22	AI606963	AI606963 vw36f02.x
	31	13.2	88.0	271	146	BF228467	BF228467 BP250008B
C	32	13.2	88.0	275	134	BA461437	BA461437 BB461437
	33	13.2	88.0	275	138	BE631643	BE631643 BE631643
C	34	13.2	88.0	276	4	AA288582	AA288582 mp15905.r
	35	13.2	88.0	276	168	BF714534	BF714534 mab01e01.
C	36	13.2	88.0	280	146	BF290833	BF290833 EST455424
	37	13.2	88.0	283	240	AZ227737	AZ227737 RPCI-23-8
C	38	13.2	88.0	285	158	H34301	H34301 EST111113.R
	39	13.2	88.0	286	157	F21363	F21363 HSPD05876.H
C	40	13.2	88.0	287	147	BF363285	BF363285 CM2-NN011
	41	13.2	88.0	288	143	BF010839	BF010839 NXCI-095
C	42	13.2	88.0	289	14	AA963063	AA963063 UI-R-E1-f
	43	13.2	88.0	295	171	BF931642	BF931642 IL2-NT020
C	44	13.2	88.0	296	12	AA822320	AA822320 vw36f02.r
	45	13.2	88.0	296	20	AI465630	AI465630 vw36f02.y

ALIGNMENTS

RESULT 1						
AA644792	AA644792	100 bp	mRNA	EST	28-OCT-1997	
LOCUS	vs82d07.r1	Barstead mouse myotubes MPLRB5	Mus musculus	cdna clone		
DEFINITION	IMAGE:1152781.5'	similar to gb:M80359	PUTATIVE			
	SERINE/THREONINE-PROTEIN KINASE P78 (HUMAN);	gb:X70764	M.musculus			
	mRNA for serine/threonine protein kinase (MOUSE);					
ACCESSION	AA644792					
VERSION	AA644792.1	GI:2571221				
KEYWORDS	EST.					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
	1 (bases 1 to 100)					
	Matra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,					
	Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,					

TITLE
JOURNAL
COMMENT

The WashU-HIMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HIMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:625989
Trace considered overall poor quality
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..100
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/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:1152781"
/clone_lib="Barstead mouse myotubes MPLRB5"
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/lab_host="DH10B"
/note="vector: pRT3B-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACGAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATCGATCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pRT3 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."

FEATURES

BASE COUNT 24 a 27 c 29 g 20 t
ORIGIN
Query Match 88.0%; Score 13.2; DB 10; Length 100;
Best Local Similarity 80.0%; Pred. No. 5, 1e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RCTCCANGRCCTCCA 15
:|||||:|||||
Db 48 GCTCCATGCACTCCA 62
RESULT 2
AI371456/c 151 bp mRNA EST 15-FEB-1999
LOCUS qy06c02.x1 NCI_CGAP_Brn23 Homo sapiens cdna clone IMAGE:2011202.3',
DEFINITION mRNA sequence.
ACCESSION AI371456
VERSION AI371456.1 GI:4150209
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 151)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTCAP), Tumor Gene Index
Unpublished (1998)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:22:14 ; Search time 3770.35 seconds
(without alignments)
37.607 Million cell updates/sec

Title: US-09-532-263-9

Perfect score: 15

Sequence: 1 RCTCCANGGRCCTCCA 15

Scoring table: IDENTITY_NUC

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Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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BASE COUNT 322 a 280 c 329 g 255 t 1 others
ORIGIN

Query Match 92.0%; Score 13.8; DB 93; Length 1187;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCTCCAYTTRCTCCA 15
:|||||:|||||
Db 849 GCTCCACTTGCTCCA 835

RESULT 15
AF072549 AF072549 1290 bp mRNA VRT 15-AUG-1998
LOCUS
DEFINITION Danio rerio transcription factor (Pax8) mRNA, partial cds.
ACCESSION AF072549
VERSION AF072549.1 GI:3420034
KEYWORDS
SOURCE zebrafish.
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasbora; Danio.
1 (bases 1 to 1290)
Pfeffer, P.L., Gerster, T., Lun, K., Brand, M. and Busslinger, M.
Characterization of three novel members of the zebrafish Pax2/5/8
family: dependency of Pax5 and Pax8 expression on the Pax2.1 (noi)
function
JOURNAL Development 125 (16), 3063-3074 (1998)
MEDLINE 98337826
REFERENCE 2 (bases 1 to 1290)
AUTHORS Pfeffer, P.L. and Busslinger, M.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1998) Institute of Molecular Pathology, Dr.
Bohr-casse 7, Vienna A-1030, Austria
FEATURES
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YYETGSKPGVIGSKPKVATPKVVEIAEYKRONPTFWAWEIKDRLLAEGVCDGDTV
PSVSSINRIIRTKVQKPNLPDFTKGLSPGHTLIPSSAVTPPESQSDSLGTSYING
LLGITQTADQKRGHDDQSCSRHSYDQSGGSGARKQLRTHFFPSAALDCGFERHY
SSDSFSQSKAEQQLYPLALMNPGLDEKGASSISRNLAHQGYAVVTEALQPLPLCLK

```
REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 1063)
TITLE Members of the Mouse retrovirus-related repetitive sequence MUERV
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1063)
AUTHORS Hardies,S.C.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1998) Biochemistry, Univ. of Texas Health Science
Center at San Antonio, 7703 Floyd Curl Dr., San Antonio, TX 78284,
USA
FEATURES Location/Qualifiers
source 1..1063
/organism="Mus musculus domesticus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="M8"
repeat_region <1..>1063
/note="similar to the gag-pol of Moloney Murine Leukemia
virus"
/rpt_type="dispersed"
/rpt_family="MuERV"
BASE COUNT 347 a 196 c 297 g 223 t
ORIGIN
Query Match 92.0%; Score 13.8; DB 94; Length 1063;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 RCTCCAYTTRCTCCA 15
:||||:|||||
Db 79 ACTCCATTGCTCCA 65
RESULT 13
MUSIL2RGAM/c
LOCUS Mouse mRNA for mouse IL-2R gamma, complete cds. 01-FEB-2000
DEFINITION Mouse mRNA for mouse IL-2R gamma, complete cds.
ACCESSION D13821
VERSION D13821.1 GI:436045
KEYWORDS IL-2 receptor; cytokine receptor family; gammachain; mouse IL-2R
gamma.
SOURCE Mus musculus (strain:C57BL/6) spleen cDNA to mRNA, clone_lib:mouse
spleen cell cDNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Kobayashi,N., Nakagawa,S., Minami,Y., Taniguchi,T. and Kono,T.
Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
gamma
JOURNAL Gene 130 (2), 303-304 (1993)
MEDLINE 93366191
REFERENCE 2 (bases 1 to 1165)
AUTHORS Taniguchi,T.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1992) to the DDBJ/EMBL/GenBank databases.
Tadatsugu Taniguchi, Osaka University, Institute for Mol. and Cell.
Biology, Suita-shi, Osaka 565, Japan (tel:06-877-5289,
Fax:06-878-9846)
COMMENT Submitted (04-DEC-1992) to DDBJ by:
Tadatsugu Taniguchi
Institute for Molecular and
Cellular Biology, Osaka University
1-3 Yamadaoka
Suita-shi, Osaka 565
Japan
Phone: 06-877-5289
Fax: 06-878-9846.
FEATURES Location/Qualifiers
source 1..1165
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="M8"
repeat_region <1..>1063
/note="similar to the gag-pol of Moloney Murine Leukemia
virus"
/rpt_type="dispersed"
/rpt_family="MuERV"
BASE COUNT 347 a 196 c 297 g 223 t
ORIGIN
Query Match 92.0%; Score 13.8; DB 94; Length 1063;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 RCTCCAYTTRCTCCA 15
:||||:|||||
Db 79 ACTCCATTGCTCCA 65
RESULT 14
HSA297692/c
LOCUS Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta chain,
exons 6-7. 30-SEP-2000
DEFINITION Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta chain,
exons 6-7.
ACCESSION AJ297692
VERSION AJ297692.1 GI:10443211
KEYWORDS IL-12 receptor beta chain; IL-12RB1 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1187)
AUTHORS Elloumi-Zghal,H., Abdelhak,S. and Dellagi,K.
TITLE Genomic structure of IL12RB1 gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1187)
AUTHORS Abdelhak,S.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2000) Abdelhak S., Immunology, Institut Pasteur
de Tunis, BP74 13, Place Pasteur, Tunis, 1002, TUNISIA
FEATURES Location/Qualifiers
source 1..1187
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/map="19p13.1"
intron 1..292
/gene="IL-12RB1"
/number=5
repeat_region 1..206
/rpt_family="Alu-Jb"
/rpt_type="DISPERSED"
gene 1..1187
/gene="IL-12RB1"
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ORIGIN

Query Match 92.0%; Score 13.8; DB 14; Length 979;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RCTCCAYTTRCTCCA 15
:|||||:|||||
Db 425 ACTCCATTACTCCA 439

RESULT 10

CEU21854 1025 bp DNA INV 14-FEB-1996
LOCUS Caenorhabditis elegans cCAF1 protein gene, complete cds.
DEFINITION U21854
ACCESSION U21854
VERSION U21854.1 GI:726133
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 1025)
Draper, M.P., Salvatore, C. and Denis, C.L.
Identification of a mouse protein whose homolog in Saccharomyces
cerevisiae is a component of the CCR4 transcriptional regulatory
complex
Mol. Cell. Biol. 15 (7), 3487-3495 (1995)
95311945
REFERENCE 2 (bases 1 to 1025)
AUTHORS Salvatore, C.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-1995) Christopher Salvatore, Biochemistry
Department, University of New Hampshire, Main Syreet, Durham, NH
03824, USA

FEATURES

source Location/Qualifiers
1..1025
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
28..960
/note="C.elegans CCR4 associated factor 1"
/codon_start=1
/product="cCAF1 protein"
/protein_id="AAA87454.1"
/db_xref="GI:726134"
/translation="MASSSGGAGGAGGAGGAGPEVKIHNVMYMSVEEFARIGFVED
YPYVMDTEFGVATPLGTFRSKEDFNQQVCNMLKLIQVGFAMVNDKGLPPT
GDVQNFNFSFADMFSHESVEMLRQAGIDFTLLQNGIPTAVFGELLTSGLTIDP
RITWLTSSGVDYGLKSLITGLDKPEESTFENCKLTLEPTFDIKILLRTPNCASA
KLKGLQEVADQLDYKRCQVHRQAGSDALLTAFTFFKIKKQFFGDNNQIAPLICGHM
FGLGSLSLFHSSTGSRUGDETPOGLIGVPQQA"
BASE COUNT 276 a 240 c 240 g 269 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 6; Length 1025;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RCTCCAYTTRCTCCA 15
:|||||:|||||
Db 80 GCTCCATTGCTCCA 66

RESULT 11

PT4G11A 1034 bp DNA PHG 28-APR-1993
LOCUS Bacteriophage T4D gene 11 encoding baseplate structural protein
DEFINITION (gp11) complete cds, gene 10, 3' end, and gene 12, 5' end.
ACCESSION M26253
VERSION M26253.1 GI:215856
KEYWORDS baseplate structural protein; gp10 gene; gp11 gene; gp12 gene.

SOURCE

ORGANISM Bacteriophage T4 DNA, clone pUz1 and pBB1.
Bacteriophage T4
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
T4-like phages.
1 (bases 1 to 1034)
Barrett, B.K. and Berget, P.B.
Laboratory methods using transposon Tn5 insertions to sequence
Bacteriophage T4 gene 11
DNA 8, 287-295 (1989)
89356257
Draft entry and computer readable copy of sequence [1] kindly
provided by P.B.Berget, 20-JUL-1989.
The reading frame for gp12 is in disagreement with Selivanov et
al., (Accession #X06792).

FEATURES

source Location/Qualifiers
1..1034
/organism="Bacteriophage T4"
/db_xref="taxon:10665"
<1..207
/note="gp10 protein"
/codon_start=1
/transl_table=11
/protein_id="AAA32493.1"
/db_xref="GI:215857"
/translation="TETDEVLIVDENGSVIVGCGQYDPEDESGPIYTKYREAKASTNS
THTPTSTINIQPVITVVRWIRIA"
207..866
/note="baseplate structural protein (gp11)"
/codon_start=1
/transl_table=11
/protein_id="AAA32494.1"
/db_xref="GI:215858"
/translation="MSLLNNKAGVISRLADFLGPRPKTGDIDVNRQSVGVTISOLA
KGFYEPNIESAINDVHNFSIKDVGTTIINTKTVSGVSGQDYWAFSGVTDDSLPPG
SPITVFLVGLPVSATGTATIEFAVKRVALQEAIASTAINSKDHPDGSKLEVY
LDNOKHVLSTYSTYGITISQEIISSEKPGYGTWNLGAQTVTLDNQQTPTVYHFERT
A"

variation

822
/note="c in wild type; t in amber mutants N108 and N93"
825
/note="c in wild type; t in amber mutants N128, NG115 and
NG369"

CDS

863..>1034
/note="gp12 protein"
/codon_start=1
/transl_table=11
/protein_id="AAA32495.1"
/db_xref="GI:553024"
/translation="MSNNTYQHSNESRYVKFDPDTDTNFPPEITDVQAAIAISPAGV
NGVPDASSTTKGI"
BASE COUNT 332 a 191 c 186 g 325 t
ORIGIN 90 kb on genomic map.

Query Match

Best Local Similarity 92.0%; Score 13.8; DB 11; Length 1034;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RCTCCAYTTRCTCCA 15
:|||||:|||||

Db 1002 ACTCCATTACTCCA 988

RESULT 12

AF064721/c 1063 bp DNA ROD 21-MAY-1998
LOCUS AF064721
DEFINITION Mus musculus domesticus clone M8 repetitive sequence MuERVc.
ACCESSION AF064721
VERSION AF064721.1 GI:3142724
KEYWORDS western European house mouse.
SOURCE Mus musculus domesticus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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BASE COUNT      203 a   181 c   168 g   193 t   3 others
ORIGIN

Query Match      92.0%; Score 13.8; DB 53; Length 748;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
    :||||:|||||
Db 46 GCTCCACTTACTCCA 32

RESULT 7
AX053546/c
LOCUS      AX053546      783 bp      DNA      PAT      13-JAN-2001
DEFINITION Sequence 312 from Patent WO0073801.
ACCESSION  AX053546
VERSION     AX053546.1 GI:12227865
KEYWORDS    human.
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 783)
AUTHORS     Obata, Y.
TITLE       Breast, gastric and prostate cancer associated antigens and uses
            therefor
JOURNAL     Patent: WO 0073801-A 312 07-DEC-2000;
            LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES    Location/Qualifiers
            source          1..783
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
BASE COUNT  255 a   147 c   160 g   216 t   5 others
ORIGIN

Query Match      92.0%; Score 13.8; DB 9; Length 783;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
    :||||:|||||
Db 98 GCTCCATTGCTCCA 84

RESULT 8
CNS01E10
LOCUS      CNS01E10      900 bp      DNA      STS      17-FEB-2000
DEFINITION Anopheles gambiae STS SP6 end of clone 02F01 of Notredame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            sequence tagged site.
ACCESSION  AL140569
VERSION     AL140569.1 GI:6998687
KEYWORDS    STS.
SOURCE      African malaria mosquito.
ORGANISM    Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
            Culicoidea; Anopheles.
REFERENCE   1 (bases 1 to 900)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            2 (bases 1 to 900)
            Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissbach, J.
            Direct Submission
            Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.

BASE COUNT      203 a   181 c   168 g   193 t   3 others
ORIGIN

Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.

FEATURES    Location/Qualifiers
            source          1..900
                        /organism="Anopheles gambiae"
                        /strain="PEST"
                        /db_xref="taxon:7165"
                        /clone="02F01"
                        /clone_lib="Notredame1"
                        /note="end : SP6"
BASE COUNT  263 a   169 c   159 g   307 t   2 others
ORIGIN

Query Match      92.0%; Score 13.8; DB 53; Length 900;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
    :||||:|||||
Db 251 GCTCCATTACTCCA 265

RESULT 9
RSM390345
LOCUS      RSM390345      979 bp      DNA      PLN      09-NOV-2000
DEFINITION Reissekia smilacina chloroplast partial trna-Leu(UAA) and trna-Phe
            genes and intergenic spacer, IGS.
ACCESSION  AJ390345
VERSION     AJ390345.1 GI:9968789
KEYWORDS    IGS; intergenic spacer; transfer RNA-Leu (UAA); transfer RNA-Phe;
            trna-Leu (UAA) gene; trna-Phe gene.
SOURCE      Reissekia smilacina.
ORGANISM    Chloroplast Reissekia smilacina
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
            Rosales; Rhamnaceae; Reissekia.
REFERENCE   1 (bases 1 to 979)
AUTHORS     Richardson, J.E., Fay, M.F., Cronk, Q.C., Bowman, D. and Chase, M.W.
TITLE       A phylogenetic analysis of Rhamnaceae using rbcL and trnL-F plastid
            DNA sequences
JOURNAL     Am. J. Bot. 87 (9), 1309-1324 (2000)
PUBMED     10991902
REFERENCE   2 (bases 1 to 979)
AUTHORS     Richardson, J.E.
TITLE       Direct Submission
JOURNAL     Submitted (28-OCT-1999) Richardson J.E., Herbarium, Royal Botanic
            Garden, Edinburgh, 20A Inverleith Row, Edinburgh, EH3 5LR, UNITED
            KINGDOM
FEATURES    Location/Qualifiers
            source          1..979
                        /organism="Reissekia smilacina"
                        /organelle="plastid:chloroplast"
                        /db_xref="taxon:106700"
                        /country="Brazil"
                        <1..596
                        /gene="trna-Leu(UAA)"
                        /product="transfer RNA-Leu(UAA)"
                        1..546
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                        547..596
                        /gene="trna-Leu(UAA)"
                        597..945
                        /note="intergenic spacer, IGS"
                        946..979
                        /gene="trna-Phe"
                        /product="transfer RNA-Phe"
                        946..979
                        /gene="trna-Phe"
BASE COUNT  339 a   184 c   169 g   287 t
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ORIGIN
Query Match          92.0%; Score 13.8; DB 95; Length 179;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
      :||||:|||||
DB 137 GCTCCACTTACTCCA 123

RESULT 4
LAU72036/c          LAU72036          271 bp          DNA          INV          30-NOV-1996
DEFINITION          Leptothorax acervorum microsatellite LXA GA 1, complete sequence.
ACCESSION           U72036
VERSION             U72036.1 GI:1695895
KEYWORDS
SOURCE
ORGANISM
Leptothorax acervorum.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Formicidae; Myrmicinae; Leptothorax.
1 (bases 1 to 271)
Bruford,M.W., Green,H.A.A. and Bourke,A.F.G.
Parentage, reproductive skew and queen turnover in a multiple-queen
ant analysed with microsatellites
unpublished
2 (bases 1 to 271)
Bruford,M.W., Green,H.A.A. and Bourke,A.F.G.
Direct Submission
TITLE
JOURNAL
Submitted (19-SEP-1996) Conservation Genetics Group, Institute of
zoology, Regent's Park, London NW1 4RY, UK
FEATURES
source
repeat_region      98..172
/db_xref="taxon:33409"
/note="LXA GA 1"
/rpt_family="microsatellite"
/rpt_type=tandem
/rpt_unit=ag
BASE COUNT          79 a 50 c 101 g 41 t
ORIGIN

Query Match          92.0%; Score 13.8; DB 6; Length 271;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
      :||||:|||||
DB 211 GCTCCACTTGTCTCCA 197

RESULT 5
AF227552/c          AF227552          487 bp          mRNA          PRI          01-JUN-2000
DEFINITION          Macaca mulatta interleukin-12 receptor (IL-12R) mRNA, partial cds.
ACCESSION           AF227552
VERSION             AF227552.1 GI:8132798
KEYWORDS
SOURCE
ORGANISM
rhesus monkey.
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
1 (bases 1 to 487)
Arredondo,J.
Cytokine Signal Transduction Genes from Rhesus Macaques
unpublished
2 (bases 1 to 487)
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE

AUTHORS              Arredondo,J.
TITLE                Direct Submission
JOURNAL              Submitted (24-JAN-2000) California Regional Primate Research
                    Center, University of California-Davis, One Shields Avenue, Davis,
                    CA 95616, USA
FEATURES
source
Location/Qualifiers
1..487
/organism="Macaca mulatta"
/db_xref="taxon:9544"
/cell_type="peripheral blood mononuclear cells"
<1..>487
/gene="IL-12R"
<1..>487
/gene="IL-12R"
/note="membrane receptor"
/codon_start=3
/product="interleukin-12 receptor"
/protein_id="AAF73397.1"
/db_xref="GI:8132799"
/translation="GPQDDPTESCLCPLENNVAQEFOLRRRLRGSGSSWSKSSPVC
VPPENPQPVRFSDVHLGRDRRLTKQPTOLELPKCGCGPARGAEVYQQLHLM
LSCPCAKATPLPLEKMPYLSGATMWLVISSNRFGLAQTRRGFLLTPTQKPEVLN
IT"
BASE COUNT          106 a 151 c 140 g 90 t
ORIGIN

Query Match          92.0%; Score 13.8; DB 89; Length 487;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
      :||||:|||||
DB 122 GCTCCACTTGTCTCCA 108

RESULT 6
CNS01KVY/c          CNS01KVY          748 bp          DNA          STS          17-FEB-2000
LOCUS               Anopheles gambiae STS sp6 end of clone 17P09 of NotreDamel library
DEFINITION          from strain PEST of Anopheles gambiae (African malaria mosquito),
                    sequence tagged site.
ACCESSION           AL148863
VERSION             AL148863.1 GI:7007009
KEYWORDS
SOURCE
ORGANISM
African malaria mosquito.
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidae; Anopheles.
1 (bases 1 to 748)
Genoscope.
Direct Submission
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
2 (bases 1 to 748)
Roth,C.W., Brey,P.T., Ke, Z., Collins,F.H. and Weissenbach,J.
Direct Submission
Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.
FEATURES
source
Location/Qualifiers
1..748
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="17P09"
/clone_lib="NotreDamel"
/note="end : Sp6"

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9	13.8	92.0	979	14	RSW390345
C 10	13.8	92.0	1025	6	CEU21854
C 11	13.8	92.0	1034	11	PTAG111A
C 12	13.8	92.0	1063	94	AF064721
C 13	13.8	92.0	1165	94	MUS1L2RGAM
C 14	13.8	92.0	1187	93	HS3297692
C 15	13.8	92.0	1290	8	AF072549
C 16	13.8	92.0	1394	94	AF047578
C 17	13.8	92.0	1410	58	AF250363
C 18	13.8	92.0	1410	58	AF250364
C 19	13.8	92.0	1429	94	BC004691
C 20	13.8	92.0	1438	59	IAU86144
C 21	13.8	92.0	1438	59	IAU86145
C 22	13.8	92.0	1458	58	FLANENJ8
C 23	13.8	92.0	1458	58	FLANANJ76
C 24	13.8	92.0	1458	59	IAU53166
C 25	13.8	92.0	1590	94	MUS1L2RGA
C 26	13.8	92.0	1608	9	AR072026
C 27	13.8	92.0	1628	94	MUS1L2RG
C 28	13.8	92.0	1623	94	MMI12RGC
C 29	13.8	92.0	1649	11	MY74G12
C 30	13.8	92.0	1655	7	AF056218
C 31	13.8	92.0	2044	5	AF077299
C 32	13.8	92.0	2100	93	HS1L12R
C 33	13.8	92.0	2104	9	AR052275
C 34	13.8	92.0	2104	9	AR059955
C 35	13.8	92.0	2104	9	AR068104
C 36	13.8	92.0	2104	10	I23702
C 37	13.8	92.0	2117	9	A68598
C 38	13.8	92.0	2117	9	AT9383
C 39	13.8	92.0	2196	12	AF056026
C 40	13.8	92.0	2232	10	E31424
C 41	13.8	92.0	2232	12	AF093241
C 42	13.8	92.0	2270	93	HSW801945
C 43	13.8	92.0	2300	12	AR097221
C 44	13.8	92.0	2309	12	AF086906
C 45	13.8	92.0	2431	8	XLFYNR

ALIGNMENTS

[illegible]

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:52:01 ; Search time 1774.1 seconds
(without alignments)
130.780 Million cell updates/sec

Title: US-09-532-263-10
Perfect score: 15
Sequence: 1 RCTCCAYTTRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba1:
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4: gb_in1:
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6: gb_in3:
7: gb_om:
8: gb_ov:
9: gb_pat1:
10: gb_pat2:
11: gb_ph:
12: gb_pl1:
13: gb_pl2:
14: gb_pl3:
15: gb_pl4:
16: gb_ba1:
17: em_ba2:
18: em_fun:
19: em_htgo_hum:
20: em_htgo_inv:
21: em_htgo_rod:
22: em_htg_hum1:
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24: em_htg_hum3:
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39: em_hum6:
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86: gb_pr2:
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88: gb_pr4:
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90: gb_pr6:
91: gb_pr7:
92: gb_pr8:
93: gb_pr9:
94: gb_ro1:
95: gb_ro2:
96: gb_in4:
97: gb_pr10:
98: em_ba3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	13.8	92.0	17	9	AR039961	AR039961 Sequence
C 2	13.8	92.0	160	94	MUSA1C2B10	M95509 Mus musculu
C 3	13.8	92.0	179	95	S7584S5	S75849 IL-2R gamma
C 4	13.8	92.0	271	6	LAU72036	U72036 Leptothorax
C 5	13.8	92.0	487	89	AF227552	AF227552 Macaca mu
C 6	13.8	92.0	748	53	CNS01KVY	AL148863 Anopheles
C 7	13.8	92.0	783	9	AX053546	AX053546 Sequence
C 8	13.8	92.0	900	53	CNS01EIO	AL140569 Anopheles

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XX 19-JUL-1993; 93US-0094649.
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PR 31-MAY-1994; 94US-0248532.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Chizzonite RA, Chua AO, Gubler UA, Truitt TP;
XX
XX WPI; 1995-076349/11.
DR P-PSDB; AAR69632.
XX
XX DNA encoding a low affinity interleukin-12 receptor - used to
PT bind or scavenge IL-12 to cause immune suppression, e.g. to
PT suppress graft-vs-host reaction, allograft rejection or
PT inflammation, and to treat autoimmune conditions
XX
XX Claim 3; Page 24-27; 61pp; English.
XX
XX A cDNA library of PHA-activated peripheral blood mononuclear cells
CC in vector pEF-BOS was screened for interleukin-12 (IL-12) receptor
CC cDNAs by panning. An isolated cDNA was sequenced (AA083844); it
CC encoded a 662-amino acid low affinity IL-12 receptor (AAR69632).
CC Recombinant IL-12 receptor was expressed in COS cells, and can be
CC used for therapeutic or diagnostic purposes.
XX
XX Sequence 2104 BP; 411 A; 624 C; 658 G; 411 T; 0 other;
SQ
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Query Match 92.0%; Score 13.8; DB 16; Length 2104;
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Search completed: August 29, 2001, 20:16:45
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QY 1 RCTCCAYTTRCTCCA 15

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Db 1223 ACTCCACTGTCTCCA 1209

RESULT 15

AAQ83844/c
ID AAQ83844 standard; cDNA to mRNA; 2104 BP.

XX

AC AAQ83844;

XX

DT 05-SEP-1995 (first entry)

XX Human interleukin-12 receptor cDNA.

DE

XX Interleukin-12 receptor; IL-12; immune suppression;

KW immunosuppressive; graft-versus-host reaction; allograft rejection;

KW inflammation; autoimmune disease; ds.

XX

OS Homo sapiens.

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Db      891 GCTCCACTTACTCCA 877
RESULT 13
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ID      AAQ71977 standard; DNA; 1608 BP.
XX
XX
AC      AAQ71977;
XX
XX      03-MAY-1995 (first entry)
DT
XX
DE      Murine IL-2R gamma gene.
XX
XX      Murine IL2-R gamma; X-linked severe combined immunodeficiency;
KW      XSCID; interleukin; ss.
XX
OS      Mus musculus.
XX
FH      Key
FT      CDS
FT      Location/Qualifiers
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FT      /*tag= a
FT      /transl_except= pos:1015..1017, aa:His
FT      sig_peptide
FT      25..82
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XX      15-SEP-1994.
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XX      10-MAR-1994; 94WO-US02891.
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XX      12-MAR-1993; 93US-0031143.
PR
XX      14-SEP-1993; 93US-0121435.
XX
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX      Leonard WJ, McBride WO, Noguchi M;
PI
XX      WPI; 1994-303046/37.
DR
XX      P-P5DB; AAR59094.
XX
XX      Diagnosis of X-linked severe combined immunodeficiency (XSCID) -
PT      this was used in the development of a claimed method for the
PT      diagnosis of X-linked severe combined immunodeficiency (XSCID),
PT      transgenic animals containing the mutated gene
XX
XX      Example 1; Fig 7; 98pp; English.
PS
XX
XX      AAQ71977 is the DNA sequence of murine IL-2R gamma AAR59094,
CC      this was used in the development of a claimed method for the
CC      diagnosis of X-linked severe combined immunodeficiency (XSCID),
CC      in female carriers and male sufferers.
XX
XX      Sequence 1608 BP; 413 A; 434 C; 349 G; 412 T; 0 other;
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Query Match      92.0%; Score 13.8; DB 15; Length 1608;
Best Local Similarity 80.0%; Pred. NO. 2.5e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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ID      AAC46177 standard; DNA; 2061 BP.
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XX      AAC46177;
AC
XX
XX      18-OCT-2000 (first entry)
DT
XX
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KW      protein identification; signal transduction pathway;
KW      metabolic pathway; promoter; termination sequence; ss.
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XX      Arabidopsis thaliana.
OS
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XX      EP1033405-A2.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 92.0%; Score 13.8; DB 21; Length 1537;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 RCTCCAYTTRCTCCA 15
:|||||:|||||

Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
:|||||:|||||
Db 803 GCTCCACTTACTCCA 789

RESULT 11

AAV26248/C
ID AAV26248 standard; DNA; 1414 BP.

AC AAV26248;

DT 24-JUL-1998 (first entry)

DE Genomic DNA SEQ ID NO:228 from WO9804684 encoding SEQ ID NO:229.

XX Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis;

KW pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;

KW Dirofilaria immitis; ss.

XX Unidentified.

OS

FH Key Location/Qualifiers

FT CDS 1..1414

FT /*tag= a

FT /note= "encodes protein given in AAW55998; a stop codon
is given in between amino acids at the end of
the protein"

XX WO9804684-A1.

XX PD 05-FEB-1998.

XX PF 25-JUL-1997; 97WO-US12212.

XX PR 25-JUL-1996; 96US-0686968.

XX PA (SYTR) SYNTRO CORP.

XX Cochran MD, Junker DE;

XX WPI; 1998-130677/12.

XX P-PSDB; AAW55998.

XX Recombinant swine pox virus - useful in vaccine for immunising

XX animal against swine pox virus

XX Disclosure; Page 402-405; 473pp; English.

XX The present sequence represents SEQ ID NO:228 from the present invention,

XX this sequence is only given in the sequence listing and is not mentioned

XX further in the specification. The present invention specifically

XX describes recombinant swinepox virus (SPV) comprising a foreign DNA (1)

XX inserted into a SPV CC genome which is capable of being expressed in a

XX host cell into which the virus is introduced, where (1) is inserted into:

XX (a) an EcoRI site within a region corresponding to a 3.2 kb subfragment

XX of the HindIII K fragment which contains both a HindIII and an EcoRI

XX site, of the SPV genome, and optionally (b) an AccI site within a region

XX corresponding to a 3.6 kb HindIII to BglII subfragment of the HindIII M

XX fragment. The recombinant SPV can be used in a vaccine for immunising an

XX animal against SPV. The invention also provides a method for testing a

XX swine to determine whether the swine has been vaccinated with the

XX vaccine, particularly containing S-SPV-008, or is infected with a

XX naturally occurring wild-type pseudorabies virus. Also (1) inserted into

XX recombinant SPV can be used in a diagnostic assay, e.g. Feline

XX immunodeficiency virus (FIV) env and gag genes and Dirofilaria immitis

XX p39 and 22kd are useful to detect feline immunodeficiency caused by FIV

XX and to detect heartworm caused by D. immitis respectively.

XX Sequence 1414 BP; 463 A; 253 C; 324 G; 374 T; 0 other;

Query Match 92.0%; Score 13.8; DB 19; Length 1414;
Best Local Similarity 80.0%; Pred No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
:|||||:|||||
Db 1037 ACTCCATTGCTCCA 1023

RESULT 12

AAC36394/C

ID AAC36394 standard; DNA; 1537 BP.

XX AAC36394;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 13639.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0129845.

XX PR 19-APR-1999; 99US-0130077.

XX PR 21-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 28-APR-1999; 99US-0130891.

XX PR 30-APR-1999; 99US-0132048.

XX PR 04-MAY-1999; 99US-0132407.

XX PR 05-MAY-1999; 99US-0132484.

XX PR 06-MAY-1999; 99US-0132486.

XX PR 06-MAY-1999; 99US-0132487.

XX PR 11-MAY-1999; 99US-0132863.

XX PR 14-MAY-1999; 99US-0134256.

XX PR 14-MAY-1999; 99US-0134218.

XX PR 14-MAY-1999; 99US-0134219.

XX PR 14-MAY-1999; 99US-0134221.

XX PR 14-MAY-1999; 99US-0134370.

XX PR 18-MAY-1999; 99US-0134768.

XX PR 19-MAY-1999; 99US-0134941.

XX PR 20-MAY-1999; 99US-0135124.

XX PR 21-MAY-1999; 99US-0135353.

XX PR 24-MAY-1999; 99US-0135629.

XX PR 25-MAY-1999; 99US-0136021.

XX PR 27-MAY-1999; 99US-0136392.

XX PR 28-MAY-1999; 99US-0136782.

XX PR 01-JUN-1999; 99US-0137222.

XX PR 03-JUN-1999; 99US-0137528.

XX PR 07-JUN-1999; 99US-0137503.

XX PR 08-JUN-1999; 99US-0137724.

XX PR 10-JUN-1999; 99US-0138094.

XX PR 10-JUN-1999; 99US-0138540.

PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match

92.0%; Score 13.8; DB 21; Length 1290;

QY 1 RCTCCAYTTRCTCCA 15
AAZ24836/c
:||||:|||||
Db 98 GCTCCATTGCTCCA 84

RESULT 9
AAZ24836/c
ID AAZ24836 standard; DNA; 1217 BP.
XX
AC AAZ24836;
XX
DT 02-DEC-1999 (first entry)
XX
DE Human secreted protein gene 26 clone HPMP40.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX W09947540-A1.

XX 23-SEP-1999.

XX 18-MAR-1999; 99WO-US05804.

PR 19-MAR-1998; 98US-0078563.

PR 19-MAR-1998; 98US-0078566.

PR 19-MAR-1998; 98US-0078573.

PR 19-MAR-1998; 98US-0078574.

PR 19-MAR-1998; 98US-0078576.

PR 19-MAR-1998; 98US-0078577.

PR 19-MAR-1998; 98US-0078578.

PR 19-MAR-1998; 98US-0078579.

PR 19-MAR-1998; 98US-0078581.

PR 01-APR-1998; 98US-0080312.

PR 01-APR-1998; 98US-0080313.

PR 01-APR-1998; 98US-0080314.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;

PI Wei Y, Endress GA, Duan RD, Kyaw H, Ebner R, Lafleur DW;

PI Olsen HS, Shi Y, Moore PA;

XX WPI: 1999-562050/47.

DR P-PSDB; AAY41333.

XX New isolated human genes, useful for diagnosis and treatment of e.g.

XX cancers, neurological disorders, immune diseases, inflammation or blood

XX disorders

XX Claim 1: Page 314; 484pp; English.

XX This sequence represents a nucleic acid molecule which encodes a

XX secreted human protein. The gene number, and the clone it is derived

CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAZ24811 for described uses).
XX
SQ Sequence 1217 BP; 346 A; 232 C; 223 G; 416 T; 0 other;

Query Match 92.0%; Score 13.8; DB 20; Length 1217;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
:||||:|||||
Db 1076 ACTCCACTTGCTCCA 1062

RESULT 10
AAC48659/c
ID AAC48659 standard; DNA; 1290 BP.

XX AAC48659;

XX AAC48659;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 58287.

XX Arabidopsis thaliana.

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XX Arabidopsis thaliana.

CC allergy and other inflammatory conditions. The ribozymes are also used
CC to induce tolerance in a recipient to alloantigen from a donor.

XX Sequence 17 BP; 6 A; 1 C; 7 G; 3 U; 0 other;

Query Match 92.0%; Score 13.8; DB 19; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:|||||
Db 17 GCTCCATTACTCCA 3

RESULT 7
AA89732/c
ID AAA89732 standard; cDNA; 494 BP.

XX AAA89732;

XX 08-JAN-2001 (first entry)

XX Mouse IL-3 receptor nucleotide sequence #3.

XX Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic;
KW antiallergic; antiasthmatic; nootropic; neuroprotective; anticonvulsant;
KW vulnery; asthma; inflammation; allergy; Chediak-Higashi syndrome; CHS;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
KW digestion disorder; wound healing disorder; gene therapy; ss.

OS Mus sp.

XX WO200043419-A2.

XX 27-JUL-2000.

XX 20-JAN-2000; 2000WO-US01431.

XX 20-JAN-1999; 99US-0116534.

XX 26-JAN-1999; 99US-0117274.

XX 26-JAN-1999; 99US-0117308.

XX 26-JAN-1999; 99US-0117309.

XX 26-JAN-1999; 99US-0117312.

XX 01-FEB-1999; 99US-0118177.

XX 01-FEB-1999; 99US-0118178.

XX 01-FEB-1999; 99US-0118179.

XX 09-FEB-1999; 99US-0119286.

XX 11-FEB-1999; 99US-0119998.

XX 11-FEB-1999; 99US-0119759.

XX (RIGE-) RIGEL PHARM INC.

XX Luo Y;

XX WPI; 2000-482908/42.

XX New nucleic acids encoding Exo proteins which are useful in the
PT diagnosis, treatment or prevention of exocytosis-mediated disorders
PT such as asthma, inflammation and allergies.

XX Disclosure; Page 302-303; 305pp; English.

XX The present sequence encodes a polypeptide which is associated with
CC the exocytosis pathway. cDNA molecules encoding proteins involved in
CC exocytosis have been isolated by yeast one-hybrid and two-hybrid
CC screening. Novel proteins, termed Exo proteins, have been identified that
CC interact with known exocytosis-associated proteins such as GS27, alpha
CC snap, unc18-1, vamps, snap-23, and the rab family of proteins.

CC Exo proteins and their agonists and antagonists are useful in the
CC diagnosis, treatment or prevention of exocytosis-mediated disorders
CC such as asthma, inflammation, allergies, Chediak-Higashi Syndrome
CC (CHS), Alzheimer's disease, Parkinson's disease, Huntington's disease,

CC diabetes, digestion disorders and wound healing disorders.
CC The nucleic acids, antagonists or agonists of Exo proteins are useful
CC in gene therapy. The nucleic acids are also useful for generating
CC transgenic or knock-out animals which can be used in the
CC development and screening of therapeutically useful reagents.

XX Sequence 494 BP; 125 A; 135 C; 129 G; 101 T; 4 other;

Query Match 92.0%; Score 13.8; DB 21; Length 494;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:|||||
Db 231 GCTCCACTTGCTCCA 217

RESULT 8
AAF22733/c

ID AAF22733 standard; cDNA; 783 BP.

XX AAF22733;

XX 26-MAR-2001 (first entry)

XX Human gastric cancer associated antigen nucleotide sequence SEQ ID:312.

XX Human; breast cancer; gastric cancer; prostate cancer; diagnosis;

XX cancer associated antigen; cytostatic; cancer vaccine; ss.

OS Homo sapiens.

XX WO200073801-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14749.

XX 28-MAY-1999; 99US-0136526.

XX 10-SEP-1999; 99US-0153454.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Obata Y;

XX WPI; 2001-025274/03.

XX Nucleic acids encoding breast, gastric and prostate cancer associated
PT antigen precursors, useful for diagnosing and treating a condition
PT characterized by expression of an abnormal amount of a protein, e.g.
PT cancer.

XX Claim 50; Page 375-376; 799pp; English.

XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP) respectively.
CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterized by expression of an abnormal amount of a protein,
CC e.g. cancer.

XX Sequence 783 BP; 255 A; 147 C; 160 G; 216 T; 5 other;

Query Match 92.0%; Score 13.8; DB 22; Length 783;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX Homo sapiens.
XX WO9967290-A1.
PN 29-DEC-1999.
XX 23-JUN-1999; 99WO-JP03351.
XX 24-JUN-1998; 98JP-0214720.
PR 19-OCT-1998; 98JP-0297409.
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX Nomura H, Maeda M;
PI WPI; 2000-116933/10.
XX Haemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders.
XX Example 1; Page 44; 176pp; Japanese.
XX The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AA259258-259300 and AA290816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
XX Sequence 15 BP; 5 A; 1 C; 6 G; 3 T; 0 other;
SQ

Query Match 92.0%; Score 13.8; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 RCTCCAYTTTCCTCCA 15
DB 15 GCTCCATTACTCTCA 1

RESULT 5
AAZ90914/C
ID AA290914 standard; DNA; 15 BP.
XX
AC AA290914;
XX
DT 24-MAY-2000 (first entry)
XX
DE Human NR8 gene probe #142.
XX
KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX Homo sapiens.
XX WO9967290-A1.
PN 29-DEC-1999.
XX 23-JUN-1999; 99WO-JP03351.
XX 24-JUN-1998; 98JP-0214720.
PR 19-OCT-1998; 98JP-0297409.
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PA

PI Nomura H, Maeda M;
XX WPI; 2000-116933/10.
XX Haemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders.
PT Example 1; Page 45; 176pp; Japanese.
XX
XX The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AA259258-259300 and AA290816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
XX Sequence 15 BP; 4 A; 1 C; 7 G; 3 T; 0 other;
SQ

Query Match 92.0%; Score 13.8; DB 21; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 RCTCCAYTTTCCTCCA 15
DB 15 ACTCCACTTGTCTCCA 1

RESULT 6
AAV94975/C
ID AAV94975 standard; RNA; 17 BP.
XX
AC AAV94975;
XX
DT 24-FEB-1999 (first entry)
XX
DE Mouse IL-2 receptor g-chain substrate position 725.
XX
KW Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
KW autoimmune disease; psoriasis; allergy; inflammatory disease;
KW graft rejection; ss.
XX
OS Mus sp.
XX
PN WO9824913-A2.
XX
PD 11-JUN-1998.
XX
PF 02-DEC-1997; 97WO-US21748.
XX
PR 03-DEC-1996; 96US-0758306.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen JA, Stinchcomb DT;
XX
XX WPI; 1998-333332/29.
XX
XX Ribozymes targeted to interleukin 2 - useful for treating e.g. cancer, autoimmune disease and allergies
XX
PS Claim 4; Page 42; 61pp; English.
XX
XX The present sequence invention describes ribozymes targeted to modulate the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA. AAV93889 to AAV94574 represent specifically claimed ribozymes, and AAV94575 to AAV95260 represent specifically claimed substrate sequences from the present invention. The ribozymes can be used for the treatment of, e.g. graft rejection, autoimmune disease, cancer, psoriasis,

PS Claim 12; Page 52; 87pp; English.
 CC 5 Degenerate hybridisation probes (AA17870-74) are based on a
 CC conserved motif (AAR92812) found in haemopoietin receptors. The
 CC probes are used in the identification and/or cloning of genes
 CC coding for novel haemopoietin receptors, e.g. the murine
 CC interleukin-11 (IL-11) receptor alpha chain gene (AA17868). Such
 CC receptors are defined by their ability to hybridise to the
 CC probes under medium stringency conditions.
 XX
 SQ Sequence 15 BP; 2 A; 6 C; 0 G; 4 T; 3 other;

Query Match 92.0%; Score 13.8; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
 :|||||:|||||
 Db 1 rctccaytttrctcca 15

RESULT 2
 AAZ90859/c
 ID AAZ90859 standard; DNA; 15 BP.

XX AAZ90859;
 AC
 XX 24-MAY-2000 (first entry)
 DT
 XX Human NR8 gene probe #87.
 DE
 XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder; fusion protein; probe; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO9967290-A1.
 PN
 XX 29-DEC-1999.
 PD
 XX 23-JUN-1999; 99WO-JP03351.
 PF
 XX 24-JUN-1998; 98JP-0214720.
 PR
 XX 19-OCT-1998; 98JP-0297409.
 XX

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 XX Nomura H, Maeda M;
 PI
 XX WPI; 2000-116933/10.
 DR
 XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders -
 XX
 XX Example 1; Page 42; 176pp; Japanese.
 PS
 XX The invention relates to the isolation of sequences encoding human
 CC haemopoietin receptor protein family NR8 genes. The NR8 family
 CC sequences were initially searched for comparison on a nucleic acid
 CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
 CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 CC AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
 CC sequences used in the search. Antibodies to the NR8 family proteins are
 CC used for the diagnosis of blood formation disorders. Compounds identified
 CC as binding to the proteins are used for the treatment of such disorders.
 CC
 XX Sequence 15 BP; 5 A; 1 C; 6 G; 3 T; 0 other;

Query Match 92.0%; Score 13.8; DB 21; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
 :|||||:|||||
 Db 1 rctccaytttrctcca 15

RESULT 4
 AAZ90907/c
 ID AAZ90907 standard; DNA; 15 BP.

XX AAZ90907;
 AC
 XX 24-MAY-2000 (first entry)
 DT
 XX Human NR8 gene probe #135.
 DE
 XX

QY 1 RCTCCAYTTRCTCCA 15
 :|||||:|||||
 Db 15 ACTCCATTGCTCCA 1

RESULT 3
 AAZ90874/c
 ID AAZ90874 standard; DNA; 15 BP.

XX AAZ90874;
 AC
 XX 24-MAY-2000 (first entry)
 DT
 XX Human NR8 gene probe #102.
 DE
 XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder; fusion protein; probe; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO9967290-A1.
 PN
 XX 29-DEC-1999.
 PD
 XX 23-JUN-1999; 99WO-JP03351.
 PF
 XX 24-JUN-1998; 98JP-0214720.
 PR
 XX 19-OCT-1998; 98JP-0297409.
 XX

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 XX Nomura H, Maeda M;
 PI
 XX WPI; 2000-116933/10.
 DR
 XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders -
 XX
 XX Example 1; Page 43; 176pp; Japanese.
 PS
 XX The invention relates to the isolation of sequences encoding human
 CC haemopoietin receptor protein family NR8 genes. The NR8 family
 CC sequences were initially searched for comparison on a nucleic acid
 CC database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
 CC the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences
 CC AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe
 CC sequences used in the search. Antibodies to the NR8 family proteins are
 CC used for the diagnosis of blood formation disorders. Compounds identified
 CC as binding to the proteins are used for the treatment of such disorders.
 CC
 XX Sequence 15 BP; 5 A; 0 C; 6 G; 4 T; 0 other;

Query Match 92.0%; Score 13.8; DB 21; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15
 :|||||:|||||
 Db 15 ACTCCATTGCTCCA 1

RESULT 4
 AAZ90907/c
 ID AAZ90907 standard; DNA; 15 BP.

XX AAZ90907;
 AC
 XX 24-MAY-2000 (first entry)
 DT
 XX Human NR8 gene probe #135.
 DE
 XX

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: August 29, 2001, 20:16:43 ; Search time 301.32 Seconds
(without alignments)
31.258 Million cell updates/sec

Title: US-09-532-263-10
Perfect score: 15
Sequence: 1 RCTCCAYTTRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseqn/NA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseqn/NA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseqn/NA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseqn/NA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseqn/NA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseqn/NA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseqn/NA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseqn/NA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseqn/NA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseqn/NA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseqn/NA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseqn/NA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseqn/NA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseqn/NA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseqn/NA1996.DAT.*
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19: /SID88/gcgdata/geneseq/geneseqn/NA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseqn/NA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseqn/NA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	
1	13.8	92.0	15	AA117874	Haemopoietin recep	
2	13.8	92.0	15	AAZ90859	Human NR8 gene pro	
3	13.8	92.0	15	AAZ90874	Human NR8 gene pro	
4	13.8	92.0	15	AAZ90907	Human NR8 gene pro	
5	13.8	92.0	15	AAZ90914	Human NR8 gene pro	
6	13.8	92.0	17	AAV94975	Mouse IL-2 recepto	
7	13.8	92.0	494	21	AAAB89732	Mouse IL-3 recepto
8	13.8	92.0	783	22	AAF22733	Human gastric canc
9	13.8	92.0	1217	20	AAZ24836	Human secreted pro
10	13.8	92.0	1290	21	AAC48659	Arabidopsis thalia
11	13.8	92.0	1414	19	AAV26248	Genomic DNA SEQ ID

C 12	13.8	92.0	1537	21	AAC36394	Arabidopsis thalia
C 13	13.8	92.0	1608	15	AAQ71977	Murine IL-2R gamma
C 14	13.8	92.0	2061	21	AAC46177	Arabidopsis thalia
C 15	13.8	92.0	2104	16	AAQ83844	Human interleukin-
C 16	13.8	92.0	2104	18	AAT59732	Human interleukin-
C 17	13.8	92.0	2104	21	AAAI1001	Human interleukin-
C 18	13.8	92.0	2117	19	AAV16362	cDNA sequence of t
C 19	13.8	92.0	2204	21	AAZ29279	A. thaliana Ethyle
C 20	13.8	92.0	2232	21	AAZ57348	Gravtropism stimu
C 21	13.8	92.0	2299	17	AAT11640	Murine osteogenic
C 22	13.8	92.0	2300	21	AAA59898	Murine DNA sequenc
C 23	13.8	92.0	2408	21	AAZ52490	Human secreted pro
C 24	13.8	92.0	3182	13	AAQ25799	hLIF-R. Homo sapi
C 25	13.8	92.0	3182	14	AAQ42590	Human LIF-R N-term
C 26	13.8	92.0	3182	15	AAQ58425	Human LIF-R clone
C 27	13.8	92.0	3182	15	AAQ55940	Human leukaemia in
C 28	13.8	92.0	3591	15	AAQ58427	Human LIF-R. Homo
C 29	13.8	92.0	3591	15	AAQ55942	Human leukaemia in
C 30	13.8	92.0	3591	16	AAQ92272	Human leukaemia in
C 31	13.8	92.0	3980	21	AAZ57349	Gravtropism stimu
C 32	13.8	92.0	7072	21	AAZ29278	A. thaliana Ethyle
C 33	13.2	88.0	15	19	AAV49499	WSXWS degenerate p
C 34	13.2	88.0	30	22	AAF76707	Human PRP PEST cod
C 35	13.2	88.0	50	21	AAZ47151	Liposome membrane-
C 36	13.2	88.0	194	21	AAA41744	Human secreted exp
C 37	13.2	88.0	436	21	AAC01348	Human secreted pro
C 38	13.2	88.0	480	21	AAC01349	Human secreted pro
C 39	13.2	88.0	618	21	AAC43764	Zea mays DNA fragm
C 40	13.2	88.0	762	21	AAA26722	Candida albicans p
C 41	13.2	88.0	1485	21	AAC42934	Arabidopsis thalia
C 42	13.2	88.0	1569	21	AAC36662	Arabidopsis thalia
C 43	13.2	88.0	151826	21	AAF22291	BAC containing rep
C 44	12.8	85.3	17	19	AAT94135	Probe 9560 for hae
C 45	12.8	85.3	30	20	AAZ87693	Human TPST-1 cDNA

ALIGNMENTS

RESULT 1
AAT17874
ID AAT17874 standard; DNA; 15 BP.
XX
AC AAT17874;
XX
DT 21-MAY-1996 (first entry)
XX
DE Haemopoietin receptor probe HYB5.
XX
KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
XX therapy; diagnosis; probe; hybridisation; ss.
OS Synthetic.
PN WO9607737-Al.
XX
PD 14-MAR-1996.
XX
PF 05-SEP-1995; 95WO-AU00578.
XX
PR 05-SEP-1994; 94AU-0007902.
PR 05-SEP-1994; 94AU-0007901.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Hilton DJ;
XX
XX WPI; 1996-171612/17.
XX
XX Nucleic acid encoding haemopoietin receptor containing conserved
XX amino acid motif esp. IL-11 receptor alpha chain - used for
XX developing IL-11 (ant)agonists

L., Durbin, R.K., Green, P., Showkeen, R., Halloran, N., Hawkins, T., Wilson, R., Berks, M., Du, Z., Thomas, K., Thierry-Mieg, J. and Sulston, J.
A survey of expressed genes in *Caenorhabditis elegans*
Nature Genet. 1, 114-123 (1992)

TITLE JOURNAL MEDLINE COMMENT

Contact: Waterston R.H.(USA) and Sulston J.E.(UK)
(USA) Dept. of Genetics or (UK)
(USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of Molecular Biology
Box 8232, 4566 Scott Ave., St. Louis, MI 63110, USA, or, Hills Road, Cambridge CB2 2QH, UK
Tel: (USA) (314)3627072 or (UK) (0223)248011
Fax: (USA) (314)3624137 or (UK) (0223)402008
Email: rv@nematode.wustl.edu or jes@mrc-lmba.cambridge.ac.uk
Single read.

FEATURES source

Location/Qualifiers
1. .324
/organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db_xref="taxon:6239"
/clone="cm2if10"
/clone_lib="Chris Martin sorted cDNA library"
/lab_host="MC1061"
/note="Vector: Mixed stage hermaphrodite cDNA library. Partially normalized by successively picking groups of clones that didn't hybridize to previously picked clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)) Host: MC1061"
96 a 54 c 89 g 77 t 8 others

BASE COUNT ORIGIN

Query Match 92.0%; Score 13.8; DB 159; Length 324;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:|||||
Db 80 GCTCCACTTGCTCCA 66

RESULT 15 BF936011/c

LOCUS BF936011 324 bp mRNA EST 22-JAN-2001
DEFINITION IL2-NT0198-291-B05 NT0198 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF936011
VERSION BF936011.1 GI:12353335
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 324)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663

JOURNAL MEDLINE COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0198-291200-291-B05&t3=2000-12-29&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 72.

FEATURES source

Location/Qualifiers
1. .324
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0198"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
55 a 128 c 84 g 56 t 1 others

BASE COUNT ORIGIN

Query Match 92.0%; Score 13.8; DB 171; Length 324;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15
:|||||:|||||
Db 98 GCTCCACTTGCTCCA 84

Search completed: August 29, 2001, 19:22:20
Job time: 24143 sec

contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTTTTN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTTAATAATATCCGCCGCCGCC 3']. cDNA was cleaved with XhoI and BamHI."

BASE COUNT 74 a 57 c 96 g 60 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 161; Length 287;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTCTCCA 15
Db 150 ACTCCATTGCTCCA 136

RESULT 12
B75501/c
LOCUS B75501 291 bp DNA GSS 08-APR-1999
DEFINITION RPCI11-16K9-TV RPCI-11 Homo sapiens genomic clone RPCI-11-16K9, DNA sequence.

ACCESSION B75501
VERSION B75501.1 GI:2771188
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 291)
AUTHORS Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden ,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter ,J.C.

TITLE Use of BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: RPCI11-16K9.TP
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadam@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES
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/db_xref="GB:7506008"
/db_xref="taxon:9606"
/clone="RPCI-11-16K9"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
76 a 70 c 95 g 50 t

BASE COUNT 76 a 70 c 95 g 50 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 256; Length 291;

Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTCTCCA 15
Db 65 GCTCCACTTGCTCCA 51

RESULT 13
B40700
LOCUS B40700 305 bp DNA GSS 18-OCT-1997
DEFINITION HS-1052-AL-E09-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate-CT 774 Col-17 Row-I, DNA sequence.

ACCESSION B40700
VERSION B40700.1 GI:2544952
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 305)
AUTHORS Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
TITLE Construction of a Characterized Clone Resource for Genomic Tagged Connectors
JOURNAL Unpublished (1997)
COMMENT Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackrone@u.washington.edu
Sequence Tagged Connector
Plate: CT 774 row: I column: 17
Class: BAC ends
High quality sequence stop: 305.

FEATURES
source
1..305
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-CT 774 Col-17 Row-I"
/clone_lib="CIT Human Genomic Sperm Library C"
/sex="M"
/note="Origin: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"
76 a 63 c 62 g 104 t
BASE COUNT 76 a 63 c 62 g 104 t
ORIGIN

Query Match 92.0%; Score 13.8; DB 256; Length 305;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTCTCCA 15
Db 260 ACTCCATTGCTCCA 274

RESULT 14
M89352/c
LOCUS M89352 324 bp mRNA EST 16-SEP-1992
DEFINITION CEL21F10 Chris Martin sorted cDNA library Caenorhabditis elegans cDNA clone cm21f10 5', mRNA sequence.

ACCESSION M89352
VERSION M89352.1 GI:275857
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 324)
AUTHORS Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A., Hillier

	Matches	12; Conservative	3; Mismatches	0; Indels	0; Gaps	0;
Qy	1	1 RCTCCAYTTRCTCCA	15			
		: :				
Db	3	3 ACTCCACTTGCTCCA	17			
RESULT	11					
BB585089/c						
LOCUS		BB585089	287 bp	EST	30-NOV-2000	
DEFINITION		BB585089 RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck Mus musculus cDNA clone 9430004A04 5', mRNA sequence.				

VERSION	BE585089.1	GI:11481633
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	mouse musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 287)	
AUTHORS	Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodojima, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, Y., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toyota, T., Wachihi, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Riken Mouse ESTs (Aizawa, K. et al. 2000)	

URL:<http://genome.rtc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermozabilization and thermoactivation of the thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Kitesuna, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken


```
RESULT 5
CNS032CC/c 215 bp DNA GSS 15-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
DEFINITION 206N11 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL224661.1 GI:7883532
VERSION AL224661.1
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 215)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 215)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 215)
Direct Submission
Genoscope.
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end and sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
source
1..215
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="206N11"
/clone_lib="G"
/note="Genoscope sequence ID : COAG206CG06SP1-end :
PUC-Ori"
BASE COUNT 46 a 58 c 63 g 43 t 5 others
ORIGIN
Query Match 92.0%; Score 13.8; DB 220; Length 215;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ROTCCAYTTRCTCCA 15
Db 169 GCTCCACTTGCTCCA 155
:||||:|||||
RESULT 6
R74725/c 216 bp mRNA EST 25-JUL-1996
LOCUS MDR0891R Mouse brain, Stratagene Mus musculus cDNA 5'end, mRNA
DEFINITION sequence.
ACCESSION R74725
VERSION R74725.1 GI:849928
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 216)
Beier,D. and Brady,K.
Mouse brain cDNAs
JOURNAL
COMMENT
Unpublished (1995)
Contact: Sikela JM
Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Fax: 3032707097
Email: nikki@tally.uchsc.edu
Seq primer: M13 Reverse.
FEATURES
source
1..216
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse brain, Stratagene"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP; Site_1: EcoRI; Site_2: Xho I;
The mouse brain library (Stratagene ) was constructed by
oligo-(dT) priming and directional cloning in Uni-ZAP XR
phage using whole brain mRNA from a Balb C post natal 20
day."
BASE COUNT 45 a 54 c 61 g 55 t 1 others
ORIGIN
Query Match 92.0%; Score 13.8; DB 188; Length 216;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ROTCCAYTTRCTCCA 15
Db 104 ACTCCACTTGCTCCA 90
:||||:|||||
RESULT 7
AA231776 231 bp mRNA EST 15-SEP-2000
LOCUS RZ612.F cDNA from rice Oryza sativa cDNA clone RZ612, mRNA
DEFINITION sequence.
ACCESSION AA231776
VERSION AA231776.1 GI:1854148
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 231)
VanDeynze,A.E., Sorrells,M.E., Park,W.D., Ayres,N.M., Fu,H.,
Cartinhour,S.W., Paul,E. and McCouch,S.R.
Anchor Probes for Comparative Mapping of Grass Genera
Theor. Appl. Genet. 97, 356-369 (1998)
Contact: McCouch SR
Dept Plant Breeding
Cornell University
Ithaca, NY 14853-1901, USA
Tel: 607 255 0420
Fax: 607 255 6683
Email: srm4@cornell.edu
cDNA from rice (Oryza sativa); forward sequence of RFLP probe
RZ612. Sequence determined by Nicola M. Ayres. For mapping
information, additional citations and other related information
concerning this probe, please refer to the RiceGenes database at
http://ars-genome.cornell.edu/cgi%2dbin/WebAce/webace?db=ricegenes&
class=Marker&object=RZ612.
FEATURES
source
1..231
/organism="Oryza sativa"
/cultivar="IR36"
/db_xref="RiceGenes:RZ612"
/db_xref="taxon:4530"
/clone="RZ612"
/clone_lib="cDNA from rice"
/note="Vector: Lambda ZAP II/pBluescript; Site_1: EcoRI; A
```

High quality sequence start: 9
High quality sequence stop: 125

FEATURES

POLYA-No. Location/Qualifiers
1. .154
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Ovary 2 (OV2)"
/note="Organ: Mix of ovaries of varying immature stages from 8-week-old plants; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."
48 a 27 c 33 g 46 t

BASE COUNT

ORIGIN

Query Match 92.0%; Score 13.8; DB 174; Length 154;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15

Db 129 GCTCCACTTGCTCCA 115

RESULT 3

A0554938/c

LOCUS A0554938 186 bp DNA GSS 28-MAY-1999
DEFINITION RPCI-11-366P19-TV RPCI-11 Homo sapiens genomic clone RPCI-11-366P19
ACCESSION A0554938
VERSION A0554938.1 GI:4914115

KEYWORDS GSS.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

AUTHORS

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES

source

Location/Qualifiers
1. .186
/organism="Homo sapiens"
/db_xref="GDB:7640538"
/db_xref="taxon:9606"
/clone="RPCI-11-366P19"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
44 a 43 c 64 g 35 t

BASE COUNT

ORIGIN

Query Match 92.0%; Score 13.8; DB 230; Length 186;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15

Db 54 GCTCCACTTGCTCCA 40

RESULT 4

BE171588

LOCUS

DEFINITION

CM0-HT0548-210200-233-e07 HT0548 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE171588

VERSION BE171588.1

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 192)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-cw0-HT0548-210

200-233-e07&t3=2000-02-21&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 2

High quality sequence stop: 192.

Location/Qualifiers

1. .192

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HT0548"

/dev_stage="Adult"

/note="Organ: head, neck; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 34 a 60 c 37 g 61 t

ORIGIN

Query Match 92.0%; Score 13.8; DB 164; Length 192;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCTCCAYTTRCTCCA 15

Db 107 GCTCCACTTGCTCCA 121

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	13.8	92.0	147	1	AA038484	AA038484 mi83c09.r
2	13.8	92.0	154	174	BG159502	BG159502 OV2_5_B09
3	13.8	92.0	186	230	AQ554938	AQ554938 RPI-11-3
4	13.8	92.0	192	164	BE171588	BE171588 CMO-HT054
5	13.8	92.0	215	220	CNS032CC	AL24661 Tetraodon
6	13.8	92.0	216	188	R74725	R74725 MD0891R Mo
7	13.8	92.0	231	4	AA231776	AA231776 RZ612.F c
8	13.8	92.0	240	156	C42038	C42038 C42038 Yuji
9	13.8	92.0	248	16	A1119961	A1119961 uc23c06.f
10	13.8	92.0	272	133	BB420958	BB420958 BB420958
11	13.8	92.0	287	161	BB585089	BB585089 BB585089
12	13.8	92.0	291	256	B75501	B75501 RPI11-16K9
13	13.8	92.0	305	256	B40700	B40700 HS-1052-A1-
14	13.8	92.0	324	159	M89352	M89352 CEL21F10 Ch
15	13.8	92.0	324	171	BF936011	BF936011 IL2-NT019
16	13.8	92.0	328	138	BE650167	BE650167 UI-M-BH3-
17	13.8	92.0	341	190	W34848	W34848 mc62a03.r1
18	13.8	92.0	347	169	BF814907	BF814907 IL5-C1014
19	13.8	92.0	350	240	AZ238189	AZ238189 RPI-23-7
20	13.8	92.0	360	26	AV185887	AV185887 AV185887
21	13.8	92.0	360	26	AV192824	AV192824 AV192824
22	13.8	92.0	360	26	AV194451	AV194451 AV194451
23	13.8	92.0	360	26	AV196133	AV196133 AV196133
24	13.8	92.0	360	156	C39835	C39835 C39835 Yuji
25	13.8	92.0	360	156	C42161	C42161 C42161 Yuji
26	13.8	92.0	360	156	C42410	C42410 C42410 Yuji
27	13.8	92.0	360	156	C43142	C43142 C43142 Yuji
28	13.8	92.0	360	156	C44203	C44203 C44203 Yuji
29	13.8	92.0	360	156	C47461	C47461 C47461 Yuji
30	13.8	92.0	360	156	C48718	C48718 C48718 Yuji
31	13.8	92.0	360	157	D67866	D67866 CELK087HF
32	13.8	92.0	364	107	AV110033	AV110033 AV110033
33	13.8	92.0	370	17	AI215425	AI215425 qhl1b10.x
34	13.8	92.0	371	156	C40410	C40410 C40410 Yuji
35	13.8	92.0	372	17	AI206294	AI206294 qr26f08.x
36	13.8	92.0	372	26	AV187143	AV187143 AV187143
37	13.8	92.0	372	156	C43783	C43783 C43783 Yuji
38	13.8	92.0	373	187	R38943	R38943 yd06f12.s1
39	13.8	92.0	374	187	R38942	R38942 yd06f11.s1
40	13.8	92.0	375	26	AV187242	AV187242 AV187242
41	13.8	92.0	375	26	AV193885	AV193885 AV193885
42	13.8	92.0	375	156	C47641	C47641 C47641 Yuji
43	13.8	92.0	375	156	C48090	C48090 C48090 Yuji
44	13.8	92.0	377	26	AV193301	AV193301 AV193301
45	13.8	92.0	377	156	D41868	D41868 RICS4820A R

ALIGNMENTS

RESULT 1	
AA038484/c	
LOCUS mi83c09.r1	147 bp mRNA EST
DEFINITION IMAGE:473200 5', mRNA sequence.	28-AUG-1996
ACCESSION AA038484	
VERSION AA038484.1	GI:1513891
KEYWORDS EST.	
SOURCE house mouse.	
ORGANISM Mus musculus	
REFERENCE 1 (bases 1 to 147)	
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Giesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and	

TITLE
JOURNAL
COMMENT

Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:283944

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 130.

FEATURES
source

Location/Qualifiers
1..147
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:473200"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="vector: pT73D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Ronaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."

BASE COUNT
ORIGIN

36 a 37 c 35 g 39 t
Query Match 92.0%; Score 13.8; DB 1; Length 147;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTCCAYTTCTCCA 15
:||||:|||||

Db 134 ACTCCACTTGCTCCA 120

RESULT 2

BG159502/c
LOCUS BG159502 154 bp mRNA EST 06-FEB-2001
DEFINITION OV2_5_B09.b1_A002 Ovary 2 (OV2) Sorghum bicolor cDNA, mRNA
sequence.

ACCESSION BG159502

VERSION BG159502.1

KEYWORDS EST.

SOURCE sorghum.

ORGANISM

Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 154)

AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
L.H.

TITLE An EST database from Sorghum: ovaries of varying immature stages

JOURNAL

COMMENT Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Seq primer: JEN REV

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
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244: gb_est175:*
245: gb_est176:*
246: gb_est177:*
247: gb_est178:*
248: gb_est179:*
249: gb_est180:*
250: gb_est181:*
251: gb_est182:*
252: gb_est183:*
253: gb_est184:*
254: gb_est185:*
255: gb_est186:*
256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 19:22:17 ; Search time 3770.35 Seconds
(without alignments)
37.607 Million cell updates/sec

Title: US-09-532-263-10
Perfect score: 15
Sequence: 1 RCTCCAVTTRCTCCA 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1:	gb_est1:*
2:	gb_est2:*
3:	gb_est3:*
4:	gb_est4:*
5:	gb_est5:*
6:	gb_est6:*
7:	gb_est7:*
8:	gb_est8:*
9:	gb_est9:*
10:	gb_est10:*
11:	gb_est11:*
12:	gb_est12:*
13:	gb_est13:*
14:	gb_est14:*
15:	gb_est15:*
16:	gb_est16:*
17:	gb_est17:*
18:	gb_est18:*
19:	gb_est19:*
20:	gb_est20:*
21:	gb_est21:*
22:	gb_est22:*
23:	gb_est23:*
24:	gb_est24:*
25:	gb_est33:*
26:	gb_est34:*
27:	gb_est35:*
28:	gb_est36:*
29:	gb_est37:*
30:	gb_est38:*
31:	gb_est39:*
32:	gb_est40:*
33:	em_estba:*
34:	em_estfun:*
35:	em_esthum1:*
36:	em_esthum2:*
37:	em_esthum3:*
38:	em_esthum4:*
39:	em_esthum5:*
40:	em_esthum6:*
41:	em_esthum7:*
42:	em_esthum8:*
43:	em_esthum9:*

44:	em_esthum10:*
45:	em_esthum11:*
46:	em_esthum12:*
47:	em_esthum13:*
48:	em_esthum14:*
49:	em_esthum15:*
50:	em_esthum16:*
51:	em_esthum17:*
52:	em_esthum18:*
53:	em_esthum19:*
54:	em_esthum20:*
55:	em_esthum21:*
56:	em_esthum22:*
57:	em_esthum23:*
58:	em_esthum24:*
59:	em_esthum25:*
60:	em_esthum26:*
61:	em_esthum27:*
62:	em_esthum28:*
63:	em_estin1:*
64:	em_estin2:*
65:	em_estin3:*
66:	em_estin4:*
67:	em_estin5:*
68:	em_estom1:*
69:	em_estom2:*
70:	em_estov1:*
71:	em_estov2:*
72:	em_estpl1:*
73:	em_estpl2:*
74:	em_estpl3:*
75:	em_estpl4:*
76:	em_estpl5:*
77:	em_estpl6:*
78:	em_estpl7:*
79:	em_estpl8:*
80:	em_estpl9:*
81:	em_estpl10:*
82:	em_estro1:*
83:	em_estro2:*
84:	em_estro3:*
85:	em_estro4:*
86:	em_estro5:*
87:	em_estro6:*
88:	em_estro7:*
89:	em_estro8:*
90:	em_estro9:*
91:	em_estro10:*
92:	em_estro11:*
93:	em_estro12:*
94:	em_estro13:*
95:	em_estro14:*
96:	em_estro15:*
97:	em_estro16:*
98:	em_estro17:*
99:	em_estro18:*
100:	em_estro19:*
101:	em_estro20:*
102:	gb_est25:*
103:	gb_est26:*
104:	gb_est27:*
105:	gb_est28:*
106:	gb_est29:*
107:	gb_est30:*
108:	gb_est31:*
109:	gb_est32:*
110:	gb_est41:*
111:	gb_est42:*
112:	gb_est43:*
113:	gb_est44:*
114:	gb_est45:*
115:	gb_est46:*
116:	gb_est47:*